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OM protein - protein search, using sw model

Run on: November 23, 2005, 04:51:33 ; Search time 189 Seconds
(without alignments)
53.469 Million cell updates/sec

Title: US-09-164-223-2

Sequence: 1 PSQASSGQARMPNAPLPSCLE 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_21.*
1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*
9: geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	123	100.0	23	AA98502	AA98502 Human WT1
2	123	100.0	23	AA98503	AA98503 Mouse WT1
3	123	100.0	23	AA61834	AA61834 Human WT1
4	123	100.0	23	AA61835	AA61835 Mouse WT1
5	123	100.0	23	AA66801	AA66801 Human Wtl
6	123	100.0	23	AAU68602	AAU68602 Mouse Wtl
7	123	100.0	23	ABG33072	ABG33072 Mouse WT1
8	123	100.0	23	ABG33071	ABG33071 Human WT1
9	123	100.0	23	ADB67204	ADB67204 Human/mou
10	123	100.0	23	ADB67205	ADB67205 Human/mou
11	123	100.0	23	ADJ80437	ADJ80437 Wilm's tu
12	123	100.0	23	ADJ80438	ADJ80438 Wilm's tu
13	123	100.0	23	ADJ83357	ADJ83357 Human WT1
14	123	100.0	23	ADJ83358	ADJ83358 Murine WT
15	123	100.0	23	ADL57246	ADL57246 Mouse Wtl
16	123	100.0	23	ADL57245	ADL57245 Human Wtl
17	123	100.0	23	ADU08800	ADU08800 Human WT1
18	123	100.0	23	ADU08801	ADU08801 Mouse WT1
19	123	100.0	152	ABG33387	ABG33387 Human WT1
20	123	100.0	152	ADB67545	ADB67545 Human pro
21	123	100.0	152	ADJ80778	ADJ80778 Wilm's tu
22	123	100.0	152	ADJ83698	ADJ83698 Human WT1
23	123	100.0	152	ADL57586	ADL57586 Human Wtl
24	123	100.0	152	ADU09141	ADU09141 Human WT1

25	123	100.0	154	2	AAW47175	AAW47175 Wilm's tu
26	123	100.0	154	5	AA678445	AA678445 Amino aci
27	123	100.0	154	6	ABG71422	ABG71422 Human Wtl
28	123	100.0	210	2	AA85086	AA85086 Wilm's tu
29	123	100.0	210	2	AAW22883	AAW22883 Wilm's tu
30	123	100.0	214	5	ABG33395	ABG33395 Human WT1
31	123	100.0	214	7	ADB67597	ADB67597 Human Wtl
32	123	100.0	214	7	ADJ80830	ADJ80830 Wilm's tu
33	123	100.0	214	8	ADJ83750	ADJ83750 Human WT-
34	123	100.0	214	8	ADJ57638	ADJ57638 Human Wtl
35	123	100.0	214	8	ADU09193	ADU09193 Human WT1
36	123	100.0	256	5	ABG33384	ABG33384 Human WT1
37	123	100.0	256	7	ADB67537	ADB67537 Human Wtl
38	123	100.0	256	7	ADJ80770	ADJ80770 Wilm's tu
39	123	100.0	256	8	ADJ83690	ADJ83690 Human WT1
40	123	100.0	256	8	ADJ57578	ADJ57578 Human WT-
41	123	100.0	256	8	ADU09133	ADU09133 Human WT1
42	123	100.0	267	7	ADJ80913	ADJ80913 Wilm's tu
43	123	100.0	267	8	ADL57721	ADL57721 Human Wtl
44	123	100.0	267	8	ADU09276	ADU09276 Codon opt
45	123	100.0	270	7	ADJ80937	ADJ80937 Wilm's tu

ALIGNMENTS

RESULT 1
AA98502
ID AA98502 standard; peptide; 23 AA.
XX
AC AA98502;
XX
DT 31-JUL-2000 (first entry)
XX
DE Human Wtl peptide SEQ ID NO:2.
XX
KW Wtl; immunotherapy; immunogenic; malignant disease; cancer; leukaemia;
KW metastatic disease; mouse; human; Wilm's tumour; immune response;
KW vaccine.
XX
OS Homo sapiens.
XX
PN NO200018795-A2.
XX
PD 06-APR-2000.
XX
PF 30-SEP-1999; 99MO-US022819.
XX
PR 30-SEP-1998; 98US-00164223.
PR 25-MAR-1999; 99US-00276484.
XX
PA (CORI-) CORIXA CORP.
PA (GAIG/) GAIGER A.
XX
PI Gaiger A, Cheever M;
XX
DR WPI; 2000-293107/25.
XX
PT Novel polypeptides comprising an immunogenic portion of a native Wtl
PT polypeptide, useful for inhibiting the development of malignant diseases
PT associated with Wtl expression e.g. leukemia or cancer.
XX
PS Claim 4; Page 46; 193pp; English.
XX
CC The present invention describes polypeptides (I) comprising an
CC immunogenic portion of a native Wilm's Tumour gene product polypeptide,
CC Wtl, (or variants of the immunogenic portion retaining the ability to
CC react with Wtl-specific antisera and/or T-cell lines or clones) and
CC comprising 16 consecutive amino acids (aa) or less of a native Wtl
CC polypeptide. The polypeptides are useful therapeutically and to
CC manufacture medicaments for enhancing/inducing an immune response in
CC patients. The polypeptides, mimetics or polynucleotides can be included
CC with a carrier/excipient in pharmaceutical compositions or with a non-

CC specific immune response enhancer (e.g. an adjuvant or enhancer
 CC preferentially enhancing a T cell response) in vaccines. Pharmaceutical
 CC compositions and vaccines can be administered to human patients to
 CC enhance or induce an immune response specific for WT1 or a cell
 CC expressing WT1, useful to inhibit the development of malignant diseases
 CC associated with WT1 expression, e.g. leukemia (especially acute/chronic
 CC myeloid leukemia or acute lymphocytic leukemia) or cancer (especially
 CC breast, lung, thyroid or gastrointestinal cancer, or a melanoma).
 CC AAY98501 to AAY98811 represent polypeptide sequences, and AA13848 to
 CC AA13862 represent PCR primers, used in the exemplification of the
 CC present invention

XX Sequence 23 AA:

XX SQ

Query Match 100.0%; Score 123; DB 3; Length 23;
 Best Local Similarity 100.0%; Pred. No. 1,4e-12;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PSQASSGQARMPNAPYLPSCLE 23
 |||||
 DB 1 PSQASSGQARMPNAPYLPSCLE 23

RESULT 2
 AAY98503
 ID AAY98503 standard; peptide; 23 AA.
 AC AAY98503;
 XX
 DT 31-JUL-2000 (first entry)
 XX
 DE Mouse WT1 peptide SEQ ID NO:3.
 XX
 KW WT1; immunotherapy; immunogenic; malignant disease; cancer; leukaemia;
 KW metastatic disease; mouse; human; Wilm's tumour; immune response;
 KW vaccine.
 XX
 OS Mus musculus.
 XX
 PN WO200018795-A2.
 XX
 PD 06-APR-2000.
 XX
 PF 30-SEP-1999; 99WO-US022819.
 XX
 PR 30-SEP-1998; 98US-00164223.
 PR 25-MAR-1999; 99US-00276484.
 XX
 PA (CORI-) CORIXA CORP.
 XX (GATC/) GAIGER A.
 PI Gaiger A, Cheever M;
 XX
 DR WPI; 2000-293107/25.
 XX
 PT Novel polypeptides comprising an immunogenic portion of a native WT1
 PT polypeptide, useful for inhibiting the development of malignant diseases
 PT associated with WT1 expression e.g. leukemia or cancer.
 XX
 PS Example 3; Page 46; 193pp; English.
 XX
 CC The present invention describes polypeptides (i) comprising an
 CC immunogenic portion of a native Wilm's Tumour gene product polypeptide,
 CC WT1, (or variants of the immunogenic portion retaining the ability to
 CC react with WT1-specific antisera and/or T-cell lines or clones) and
 CC comprising 16 consecutive amino acids (aa) or less of a native WT1
 CC polypeptide. The polypeptides are useful therapeutically and to
 CC manufacture medicaments for enhancing/inducing an immune response in
 CC patients. The polypeptides, mimetics or polynucleotides can be included
 CC with a carrier/excipient in pharmaceutical compositions or with a non-
 CC specific immune enhancer (e.g. an adjuvant or enhancer
 CC preferentially enhancing a T cell response) in vaccines. Pharmaceutical
 CC compositions and vaccines can be administered to human patients to

CC enhance or induce an immune response specific for WT1 or a cell
 CC expressing WT1, useful to inhibit the development of malignant diseases
 CC associated with WT1 expression, e.g. leukemia (especially acute/chronic
 CC myeloid leukemia or acute lymphocytic leukemia) or cancer (especially
 CC breast, lung, thyroid or gastrointestinal cancer, or a melanoma).
 CC AAY98501 to AAY98811 represent polypeptide sequences, and AA13848 to
 CC AA13862 represent PCR primers, used in the exemplification of the
 CC present invention

XX Sequence 23 AA:

XX SQ

Query Match 100.0%; Score 123; DB 3; Length 23;
 Best Local Similarity 100.0%; Pred. No. 1,4e-12;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PSQASSGQARMPNAPYLPSCLE 23
 |||||
 DB 1 PSQASSGQARMPNAPYLPSCLE 23

RESULT 3
 AAG61834
 ID AAG61834 standard; peptide; 23 AA.
 AC AAG61834;
 XX
 DT 06-JUL-2001 (first entry)
 XX
 DE Human WT1 immunogenic peptide SEQ ID NO: 2.
 XX
 KW Human; mouse; immunotherapy; cancer; leukaemia; WT1; Wilm's tumour gene;
 KW chromosome 11p13; zinc finger transcription factor.
 XX
 OS Homo sapiens.
 XX
 PN WO200125273-A2.
 XX
 PD 12-APR-2001.
 XX
 PF 04-OCT-2000; 2000WO-US027465.
 XX
 PR 04-OCT-1999; 99US-0157459P.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Skeiky YAM, Xu J, Cheever MA, Reed SG;
 XX
 DR WPI; 2001-328324/34.
 XX
 PT Polypeptide comprising part of the Wilm's Tumor gene product sequence is
 PT used in the diagnosis and treatment of malignant diseases e.g. leukemia
 PT and cancer associated with WT1.
 XX
 PS Claim 4; Page 155; 228pp; English.
 XX
 CC The present invention describes compositions comprising peptides derived
 CC from the Wilm's tumour protein WT1 and methods for their use in treating
 CC malignant diseases. Peptides derived from both the murine and human WT1
 CC proteins are provided. The human WT1 gene is found on chromosome 11p13,
 CC and the protein was shown to be a zinc finger transcription factor. The
 CC immunogenic peptides of the invention are particularly useful in the
 CC diagnosis and treatment of cancer and leukaemia. The present sequence is
 CC a polypeptide described in the exemplification of the invention

XX Sequence 23 AA:

XX SQ

Query Match 100.0%; Score 123; DB 4; Length 23;
 Best Local Similarity 100.0%; Pred. No. 1,4e-12;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PSQASSGQARMPNAPYLPSCLE 23
 |||||
 DB 1 PSQASSGQARMPNAPYLPSCLE 23

```
RESULT 4
AAG61835
ID AAG61835 standard; peptide; 23 AA.
XX
XX
AC AAG61835;
XX
XX
DT 06-JUL-2001 (first entry)
XX
XX
DE Mouse Wt1 immunogenic peptide SEQ ID NO: 3.
XX
XX
KW Human; mouse; immunotherapy; cancer; leukemia; Wt1; Wilm's tumour gene;
KW chromosome 11p13; zinc finger transcription factor.
XX
XX
OS Mus musculus.
XX
XX
PN WO200125273-A2.
XX
XX
PD 12-APR-2001.
XX
XX
PF 04-OCT-2000; 2000WO-US027465.
XX
XX
PR 04-OCT-1999; 99US-0157459P.
XX
XX
PA (CORI-) CORIXA CORP.
XX
XX
PI Skelky YAW, Xu J, Cheever MA, Reed SG;
XX
XX
DR WPI; 2001-328324/34.
XX
XX
PT Polypeptide comprising part of the Wt1s Tumor gene product sequence is
PT used in the diagnosis and treatment of malignant diseases e.g. leukemia
PT and cancer associated with Wt1.
XX
XX
PS Example 3; Page 155; 228pp; English.
XX
XX
CC The present invention describes compositions comprising peptides derived
CC from the Wt1's tumour protein Wt1 and methods for their use in treating
CC malignant diseases. Peptides derived from both the murine and human Wt1
CC proteins are provided. The human Wt1 gene is found on chromosome 11p13,
CC and the protein was shown to be a zinc finger transcription factor. The
CC immunogenic peptides of the invention are particularly useful in the
CC diagnosis and treatment of cancer and leukemia. The present sequence is
CC a polypeptide described in the exemplification of the invention
CC
XX
XX
SQ Sequence 23 AA;
XX
XX
Query Match 100.0%; Score 123; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.4e-12;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX
QY 1 PSQASSGQARMFPNAPYLPSCLE 23
DB 1 PSQASSGQARMFPNAPYLPSCLE 23
XX
XX
RESULT 5
AAU68601
ID AAU68601 standard; peptide; 23 AA.
XX
XX
AC AAU68601;
XX
XX
DT 16-JAN-2002 (first entry)
XX
XX
DE Human Wilm's tumour protein, Wt1, antigenic peptide #2.
XX
XX
KW Human; Wilm's tumour; Wt1; pleural mesothelioma; antigen; leukemia;
KW acute myeloid leukemia; AML; chronic myeloid leukemia; CML;
KW acute lymphocytic leukemia; ALL; myelodysplastic syndromes;
KW myeloproliferative syndrome; cancer; cytostatic.
XX
XX
OS Homo sapiens.
XX
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XX
XX
PN WO200162920-A2.
XX
XX
PD 30-AUG-2001.
XX
XX
PF 22-FEB-2001; 2001WO-US005702.
XX
XX
PR 22-FEB-2000; 2000US-0184070P.
XX
XX
PA (CORI-) CORIXA CORP.
XX
XX
PI Cheever MA, Gaiger A;
XX
XX
DR WPI; 2001-648218/74.
XX
XX
PT Composition for the treatment of mesothelioma comprises specific peptides
PT 1.e. Wt1s' tumor antigen polypeptide derived antigenic fragments.
XX
XX
PS Claim 1; Page 24; 242pp; English.
XX
XX
CC The invention relates to the use of a composition comprising at least a
CC first isolated peptide, of between 9 and 40 amino acids or a first
CC nucleic acid, encoding the peptide, in the manufacture of a medicament
CC for treating or preventing mesothelioma. The peptides are antigenic
CC peptides derived from the Wt1s' tumour protein Wt1. The composition is
CC useful for the treatment of mesothelioma, Wilm's tumour, preferably
CC pleural mesothelioma and other Wt1 associated malignancies e.g. leukemia
CC (including acute myeloid leukemia, ALL, chronic myeloid leukemia, CML,
CC acute lymphocytic leukemia, ALL, and childhood ALL), myelodysplastic
CC syndromes, myeloproliferative syndromes and cancers (e.g. breast,
CC testicular, prostate, lung and ovarian) in mammals, preferably humans.
CC The present sequence is an antigenic peptide of the invention derived
CC from human Wt1
CC
XX
XX
SQ Sequence 23 AA;
XX
XX
Query Match 100.0%; Score 123; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.4e-12;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX
QY 1 PSQASSGQARMFPNAPYLPSCLE 23
DB 1 PSQASSGQARMFPNAPYLPSCLE 23
XX
XX
RESULT 6
AAU68602
ID AAU68602 standard; peptide; 23 AA.
XX
XX
AC AAU68602;
XX
XX
DT 16-JAN-2002 (first entry)
XX
XX
DE Mouse Wilm's tumour protein, Wt1, antigenic peptide #1.
XX
XX
KW Mouse; Wilm's tumour; Wt1; pleural mesothelioma; antigen; leukemia;
KW acute myeloid leukemia; AML; chronic myeloid leukemia; CML;
KW acute lymphocytic leukemia; ALL; myelodysplastic syndromes;
KW myeloproliferative syndrome; cancer; cytostatic.
XX
XX
OS Mus musculus.
XX
XX
PN WO200162920-A2.
XX
XX
PD 30-AUG-2001.
XX
XX
PF 22-FEB-2001; 2001WO-US005702.
XX
XX
PR 22-FEB-2000; 2000US-0184070P.
XX
XX
PA (CORI-) CORIXA CORP.
XX
XX
PI Cheever MA, Gaiger A;
XX
```

XX WPI; 2001-648218/74.

DR

XX Composition for the treatment of mesothelioma comprises specific peptides

PT i.e. Wilms' tumor antigen polypeptide derived antigenic fragments.

Pt

XX

PS Claim 1; Page 24; 24zpp; English.

XX

The invention relates to the use of a composition comprising at least a first isolated peptide, of between 9 and 40 amino acids or a first nucleic acid, encoding the peptide, in the manufacture of a medicament for treating or preventing mesothelioma. The peptides are antigenic CC peptides derived from the Wilms' tumour protein WT1. The composition is useful for the treatment of mesothelioma, Wilms' tumour, preferably pleural mesothelioma and other WT1 associated malignancies e.g. leukaemia CC (including acute myeloid leukaemia, ALL, chronic myeloid leukaemia, CML, acute lymphocytic leukaemia, ALL, and childhood ALL), myelodysplastic syndromes, myeloproliferative syndromes and cancers (e.g. breast, testicular, prostate, lung and ovarian) in mammals, preferably humans. CC The present sequence is an antigenic peptide of the invention derived from mouse WT1

CC

SQ Sequence 23 AA;

Query Match	Best Local Similarity	Score 123;	ID	DB 4;	Length 23;
MATCHES	23;	Conservative 0;	Mismatches 0;	Gaps 0;	

OY

1 PSQAASSGQARMFPNAPYLPSCLE 23
|||||
Db 1 PSQAASSGQARMFPNAPYLPSCLE 23

RESULT 7

ABG33072	strandand; peptide; 23 AA.
AC ABG33072; DT 15-JUL--2002 (first entry) DE Mouse WT1 immunogenic peptide #1. KX Human; mouse; cytostatic; immunosuppressant; WT1; cancer; immune response. OS Mus musculus. PN WO200228414-A1. PD 11-APR--2002. PF 03-OCT--2001; 2001WO-US031139. PR 06-OCT--2000; 2000US-00684361. PR 09-OCT--2000; 2000US-00685830. PR 15-FEB--2001; 2001US-00785019. PA 24-AUG--2001; 2001US-00938864. (CORI) CORIXA CORP. (GAIG) GAIGER A. GAIGER A., McNeill PD, Smithgall M, Moulton G, Vedvick TS; Sleath PR, Mossman S, Evans L, Spies AG, Boydston J; WPI; 2002-352217/38. Noval isolated WT1 polynucleotide, and encoded polypeptide, useful for treating and diagnosing cancer in a patient. Example 3; Page 165; 260pp; English. <p>CC The invention relates to an isolated WT1 polynucleotide (1) and polypeptide encoded by (1). The WT1 polynucleotides and polypeptides are</p>	

```

CC used for treating and detecting cancer in a patient, and for stimulating
CC an immune response in patient. ABG33070-ABG33405 represent WT1 amino acid
CC sequences of the invention
xx
SQ Sequence 23 AA;
Query Match 100.0%; Score 123; DB 5; Length 23;
Best Local Similarity 100.0%; Pred. NO. 1.4e-12;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PSQASSGQARMFPNAPYLPSCLE 23
1 |||||
1 PSQASSGQARMFPNAPYLPSCLE 23
DB
RESULT 8
ABG33071
ID ABG33071 standard; peptide; 23 AA.
XX
AC ABG33071;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human WT1 immunogenic peptide #2.
XX
KW Human; mouse; cytostatic; immunostimulant; WT1; cancer; immune response.
XX
OS Homo sapiens.
XX
PN WO200228414-A1.
XX
PD 11-APR-2002.
XX
PF 03-OCT-2001; 2001WO-US031139.
XX
PR 06-OCT-2000; 2000US-00684361.
PR 09-OCT-2000; 2000US-00685830.
PR 15-FEB-2001; 2001US-00785019.
PR 24-AUG-2001; 2001US-00938864.
XX
XX (CORI-) CORIXA CORP.
PA (GATG/) GAIGER A.
XX
PI Gaiger A, McNeill PD, Smithgall M, Moulton G, Vedrick TS;
PI Sleath PR, Mossman S, Evans L, Spies AG, Boydston J;
XX
DR WPI; 2002-352217/38.
XX
PT Novel isolated WT1 polynucleotide, and encoded polypeptide, useful for
PT treating and diagnosing cancer in a patient.
XX
PS Example 3; Page 165; 260pp; English.
XX
CC The invention relates to an isolated WT1 polynucleotide (I) and
CC polypeptide encoded by (I). The WT1 polynucleotides and polypeptides are
CC used for treating and detecting cancer in a patient, and for stimulating
CC an immune response in patient. ABG33070-ABG33405 represent WT1 amino acid
CC sequences of the invention
XX
SQ Sequence 23 AA;
Query Match 100.0%; Score 123; DB 5; Length 23;
Best Local Similarity 100.0%; Pred. NO. 1.4e-12;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PSQASSGQARMFPNAPYLPSCLE 23
1 |||||
1 PSQASSGQARMFPNAPYLPSCLE 23
DB
RESULT 9
ADB67204
ID ADB67204 standard; peptide; 23 AA.

```

XX ADB67204;
 AC
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Human/mouse WT1 antigenic peptide #1.
 XX
 KW Human; Wilm's tumour antigen; WT1; cytostatic; antigen; T cell;
 KM antigen-presenting cell; CD4+; CD8+; immune response; cancer; vaccine;
 XX Leukaemia; antigen.
 OS Homo sapiens.
 OS Mus musculus.
 XX US2003072767-A1.
 XX
 PD 17-APR-2003.
 XX
 PF 24-AUG-2001; 2001US-00938864.
 XX
 PR 30-SEP-1998; 98US-00164223.
 PR 25-MAR-1999; 99US-00276484.
 PR 06-OCT-2000; 2000US-00684361.
 PR 09-OCT-2000; 2000US-00685830.
 PR 15-FEB-2001; 2001US-00785019.
 XX
 PA (GAIG/) GAIGER A.
 PA (MCNE/) MCNEILL P D.
 PA (SMIT/) SMITHGALL M.
 PA (MOUT/) MOUTON G.
 PA (VEDV/) VEDVICK T S.
 PA (SLEA/) SLEATH P R.
 PA (MOSS/) MOSSMAN S.
 PA (EVAN/) EVANS L.
 PA (SPIE/) SPIES A G.
 PA (BOYD/) BOYDSTON J.
 XX
 PI Gaiger A, McNeill PD, Smithgall M, Moulton G, Vedicick TS;
 PI Sleath PR, Mosseman S, Evans L, Spies AG, Boydston J;
 XX
 DR WPI; 2003-605957/57.
 XX
 PT Novel Wilm's tumor polynucleotides encoding WT1 polypeptides, useful for
 PT detecting the presence of cancer in a patient, and in pharmaceutical
 PT compositions, e.g. vaccines, for treating cancers e.g. leukemia.
 XX
 PS Example 3; Page 20; 197pp; English.
 XX
 CC The invention relates to an isolated Wilm tumour (WT1) polynucleotide
 CC comprising a full length protein, truncated protein, mutated protein or
 CC fusion protein. Also included are the encoded WT1 proteins, expression
 CC vectors, host cells, antibodies, detecting the presence of a cancer in a
 CC patient by contacting a biological sample with a binding agent that binds
 CC to a WT1 protein, an oligonucleotide that hybridises to a WT1
 CC polynucleotide, stimulating and/or expanding T cells specific for a
 CC tumour protein by contacting T cells with the WT1 polynucleotide, the WT1
 CC protein or antigen-presenting cells that express the WT1 protein, a
 CC composition (CI) (comprising physiologically acceptable carriers and
 CC immunostimulants as first component, and a second component selected from
 CC the WT1 polynucleotide, the WT1 protein, Ab, or T cells and antigen
 CC presenting cells that express the WT1 protein), inhibiting the
 CC development of a cancer in a patient (by incubating CD4+ and/or CD8+ T
 CC cells isolated from a patient with the WT1 polynucleotide, the WT1
 CC protein or antigen presenting cells that express the WT1 protein, such
 CC that T cell proliferate, administering the proliferated T cells to the
 CC patient, and thus inhibiting the development of a cancer in the patient)
 CC and a composition (C2) (comprising a WT1 polypeptide resuspended in a
 CC buffer comprising at least 1-3 sugars selected from trehalose, maltose,
 CC sucrose, fructose and glucose, at a concentration of 7-13%, and
 CC optionally ethanolamine, cysteine and polysorbate-80, or WT1 polypeptide
 CC and MW-SE or Enhancyn). Also disclosed as new are polypeptides
 CC comprising a variant of an immunogenic portion of WT1 polypeptide. CI is
 CC useful for stimulating immune response in a patient, and for treating

CC cancer in a patient. The oligonucleotide is also useful for determining
 CC the presence of a cancer in a patient. The WT1 polynucleotide and the WT1
 CC protein are useful in pharmaceutical compositions, e.g. vaccines, the WT1
 CC protein is useful as marker to indicate the presence or absence of a
 CC cancer. CI is useful for inhibiting the development of a malignant
 CC disease in a patient, for preventing and treating metastatic diseases
 CC e.g. leukemia and cancer, and for removing tumour cells from a
 CC biological sample. Ab (binding agent for the WT1 protein) is useful for
 CC detecting the presence of cancer in a patient. The present sequence is a
 CC human WT1 antigenic peptide.
 XX
 SQ Sequence 23 AA:
 QY
 DB 1 PSQASSGQARMPNAPYLPSCLE 23
 1 PSQASSGQARMPNAPYLPSCLE 23
 RESULT 10
 ADB67205
 ID ADB67205 standard; peptide; 23 AA.
 AC
 XX ADB67205;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Human/mouse WT1 antigenic peptide #2.
 XX
 KW Human; Wilm's tumour antigen; WT1; cytostatic; antigen; T cell;
 KM antigen-presenting cell; CD4+; CD8+; immune response; cancer; vaccine;
 XX Leukaemia; antigen.
 OS Homo sapiens.
 OS Mus musculus.
 XX US2003072767-A1.
 XX
 PD 17-APR-2003.
 XX
 PF 24-AUG-2001; 2001US-00938864.
 XX
 PR 30-SEP-1998; 98US-00164223.
 PR 25-MAR-1999; 99US-00276484.
 PR 06-OCT-2000; 2000US-00684361.
 PR 09-OCT-2000; 2000US-00685830.
 PR 15-FEB-2001; 2001US-00785019.
 XX
 PA (GAIG/) GAIGER A.
 PA (MCNE/) MCNEILL P D.
 PA (SMIT/) SMITHGALL M.
 PA (MOUT/) MOUTON G.
 PA (VEDV/) VEDVICK T S.
 PA (SLEA/) SLEATH P R.
 PA (MOSS/) MOSSMAN S.
 PA (EVAN/) EVANS L.
 PA (SPIE/) SPIES A G.
 PA (BOYD/) BOYDSTON J.
 XX
 PI Gaiger A, McNeill PD, Smithgall M, Moulton G, Vedicick TS;
 PI Sleath PR, Mosseman S, Evans L, Spies AG, Boydston J;
 XX
 DR WPI; 2003-605957/57.
 XX
 PT Novel Wilm's tumor polynucleotides encoding WT1 polypeptides, useful for
 PT detecting the presence of cancer in a patient, and in pharmaceutical
 PT compositions, e.g. vaccines, for treating cancers e.g. leukemia.
 XX
 PS Example 3; Page 20; 197pp; English.
 XX

CC The invention relates to an isolated Wilm's tumour (WT1) polynucleotide
 CC comprising a full length protein, truncated protein, mutated protein or
 CC fusion protein. Also included are the encoded WT1 proteins, expression
 CC vectors, host cells, antibodies, detecting the presence of a cancer in a
 CC patient by contacting a biological sample with a binding agent that binds
 CC to a WT1 protein, an oligonucleotide that hybridizes to a WT1
 CC polynucleotide, stimulating and/or expanding T cells specific for a
 CC tumor protein by contacting T cells with the WT1 polynucleotide, the WT1
 CC protein or antigen-presenting cells that express the WT1 protein, a
 CC composition (C1) (comprising physiologically acceptable carriers and
 CC immunostimulants as first component, and a second component selected from
 CC the WT1 polynucleotide, the WT1 protein, Ab, or T cells and antigen
 CC presenting cells that express the WT1 protein), inhibiting the
 CC development of a cancer in a patient (by incubating CD4+ and/or CD8+ T
 CC cells isolated from a patient with the WT1 polynucleotide, the WT1
 CC protein or antigen presenting cells that express the WT1 protein, such
 CC that T cell proliferate, administering the proliferated T cells to the
 CC patient, and thus inhibiting the development of a cancer in the patient)
 CC and a composition (C2) (comprising a WT1 polypeptide resuspended in a
 CC buffer comprising at least 1-3 sugars selected from trehalose, maltose,
 CC sucrose, fructose and glucose, at a concentration of 7-13%, and
 CC optionally ethanolamine, cysteine and poly sorbate-80, or WT1 polypeptide
 CC and Mpl-SE or Enhanzyn). Also disclosed as new are polypeptides
 CC comprising a variant of an immunogenic portion of WT1 polypeptide. C1 is
 CC useful for stimulating immune response in a patient, and for treating
 CC cancer in a patient. The oligonucleotide is also useful for determining
 CC the presence of a cancer in a patient. The WT1 polynucleotide and the WT1
 CC protein are useful in pharmaceutical compositions, e.g. vaccines. The WT1
 CC protein is useful as marker to indicate the presence or absence of a
 CC cancer. C1 is useful for inhibiting the development of a malignant
 CC disease in a patient, for preventing and treating metastatic diseases
 CC e.g. leukemia and cancer, and for removing tumor cells from a
 CC biological sample. Ab (binding agent for the WT1 protein) is useful for
 CC detecting the presence of cancer in a patient. The present sequence is a
 CC human WT1 antigenic peptide.

SO Sequence 23 AA:

Query Match 100.0%; Score 123; DB 7; Length 23;
 Best Local Similarity 100.0%; Pred. No. 1,4e-12;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PSQASSGQARMPNAPYLPSCLE 23
 |||||
 Db 1 PSQASSGQARMPNAPYLPSCLE 23

RESULT 11

ADJ80437
 ID ADJ80437 standard; peptide; 23 AA.

AC ADJ80437;

DT 06-MAY-2004 (first entry)

DE Wilm's tumor antigen immunogenic peptide #2.

KW cytostatic; gene therapy; vaccine; Wilm's tumor antigen; WT1; cancer;
 leukemia.

OS Homo sapiens.

PN WO2003037060-A2.

PD 08-MAY-2003.

PF 30-OCT-2002; 2002WO-US035194.

PR 30-OCT-2001; 2001US-00002603.

PR 16-APR-2002; 2002US-00125635.

PR 12-JUL-2002; 2002US-00195835.

PR 16-SEP-2002; 2002US-00244830.

PA (CORI-) CORIXA CORP.
 PA (GAIG/) GAIGER A.
 PI Gaiger A, McNeill PD, Jaya N, Carter D;
 DR WPI; 2003-430453/40.
 XX
 XX
 PT New isolated polypeptide for diagnosing, preventing or treating malignant
 PT diseases, e.g. cancer or leukemia, comprises an immunogenic portion of a
 PT Wilm's tumor antigen.
 PT
 PS Disclosure; SEQ ID NO 2; 371pp; English.
 XX
 CC The invention relates to an isolated polypeptide comprising an
 CC immunogenic portion of a Wilm's tumor antigen, or its variant that
 CC differs in one or more substitutions, deletions, additions and/or
 CC insertions, such that the ability of the variant to react with WT1-
 CC specific antisera and/or T-cell lines or clones is not substantially
 CC diminished. The composition and methods are useful in diagnosing,
 CC preventing or treating malignant diseases, such as cancer or leukemia.
 CC This sequence represents a peptide of the invention.

SO Sequence 23 AA:

Query Match 100.0%; Score 123; DB 7; Length 23;
 Best Local Similarity 100.0%; Pred. No. 1,4e-12;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PSQASSGQARMPNAPYLPSCLE 23
 |||||
 Db 1 PSQASSGQARMPNAPYLPSCLE 23

RESULT 12

ADJ80438
 ID ADJ80438 standard; peptide; 23 AA.

AC ADJ80438;

DT 06-MAY-2004 (first entry)

DE Wilm's tumor antigen immunogenic peptide #3.

KW cytostatic; gene therapy; vaccine; Wilm's tumor antigen; WT1; cancer;
 leukemia.

OS Homo sapiens.

PN WO2003037060-A2.

PD 08-MAY-2003.

PF 30-OCT-2002; 2002WO-US035194.

PR 30-OCT-2001; 2001US-00002603.

PR 16-APR-2002; 2002US-00125635.

PR 12-JUL-2002; 2002US-00195835.

PR 16-SEP-2002; 2002US-00244830.

PA (CORI-) CORIXA CORP.

PA (GAIG/) GAIGER A.

PI Gaiger A, McNeill PD, Jaya N, Carter D;

DR WPI; 2003-430453/40.

PT New isolated polypeptide for diagnosing, preventing or treating malignant

PT diseases, e.g. cancer or leukemia, comprises an immunogenic portion of a

PT Wilm's tumor antigen.

PS Disclosure; SEQ ID NO 3; 371pp; English.

XX The invention relates to an isolated polypeptide comprising an

CC immunogenic portion of a Wilm's tumor antigen, or its variant that
 CC differs in one or more substitutions, deletions, additions and/or
 CC insertions, such that the ability of the variant to react with WT1-
 CC specific antisera and/or T-cell lines or clones is not substantially
 CC diminished. The composition and methods are useful in diagnosing,
 CC preventing or treating malignant diseases, such as cancer or leukemia.
 CC This sequence represents a peptide of the invention.

XX
 SQ Sequence 23 AA;

Query Match 100.0%; Score 123; DB 7; Length 23;
 Best Local Similarity 100.0%; Pred. No. 1.4e-12;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQASSGQARMPNAPYLPSCLE 23
 |||||
 DB 1 PSQASSGQARMPNAPYLPSCLE 23

RESULT 13

ID ADJ83357 standard; peptide; 23 AA.

AC ADJ83357;

DT 06-MAY-2004 (first entry)

DE Human WT1 (Wilm's tumour) immunogenic peptide - SEQ ID 2.

KW immune response; WT1; Wilm's tumour; immunostimulant; cytostatic; vaccine;
 KW malignant disease; leukaemia; cancer; human.

OS Homo sapiens.

PN US2003235557-A1.

PD 25-DEC-2003.

PF 16-SEP-2002; 2002US-00244830.

PR 30-SEP-1998; 98US-00164223.

PR 25-MAR-1999; 99US-00276484.

PR 06-OCT-2000; 2000US-00684361.

PR 09-OCT-2000; 2000US-00685830.

PR 15-FEB-2001; 2001US-00785019.

PR 24-AUG-2001; 2001US-00938864.

PR 30-OCT-2001; 2001US-00002603.

PR 16-APR-2002; 2002US-00125635.

PR 12-JUL-2002; 2002US-00195835.

PA (CORI-) CORIXA CORP.

PI Gaiger A., Cheever MA;

PS WPI; 2004-070542/07.

PT Inducing an immune response in an animal, useful for treating or

PT preventing cancer, comprises administering a composition comprising a

PT viral vector comprising an immunogenic portion of a WT1 polynucleotide.

XX Example 1; SEQ ID NO 2; 229pp; English.

XX The invention relates to a novel method for inducing an immune response

XX in an animal which involves administering a first and a second

XX composition comprising a first and a second viral vector, respectively,

XX each having at least an immunogenic portion of a WT1 (Wilm's tumour)

XX polynucleotide operably linked to an expression control sequence. The

XX method of the invention has immunostimulant and cytostatic applications

XX and may be useful for generating or enhancing an immune response to WT1,

XX possibly via the production of a vaccine, as well as for preventing

XX and/or treating malignant diseases such as leukaemia and cancer. The

XX current sequence is that of the human WT1 immunogenic peptide of the

XX invention.

XX
 SQ Sequence 23 AA;

Query Match 100.0%; Score 123; DB 8; Length 23;
 Best Local Similarity 100.0%; Pred. No. 1.4e-12;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQASSGQARMPNAPYLPSCLE 23
 |||||
 DB 1 PSQASSGQARMPNAPYLPSCLE 23

RESULT 14

ID ADJ83358 standard; peptide; 23 AA.

AC ADJ83358;

DT 06-MAY-2004 (first entry)

DE Murine WT1 (Wilm's tumour) immunogenic peptide - SEQ ID 3.

KW immune response; WT1; Wilm's tumour; immunostimulant; cytostatic; vaccine;
 KW malignant disease; leukaemia; cancer; murine; mouse.

OS Mus musculus.

PN US2003235557-A1.

PD 25-DEC-2003.

PF 16-SEP-2002; 2002US-00244830.

PR 30-SEP-1998; 98US-00164223.

PR 25-MAR-1999; 99US-00276484.

PR 06-OCT-2000; 2000US-00684361.

PR 09-OCT-2000; 2000US-00685830.

PR 15-FEB-2001; 2001US-00785019.

PR 24-AUG-2001; 2001US-00938864.

PR 30-OCT-2001; 2001US-00002603.

PR 16-APR-2002; 2002US-00125635.

PR 12-JUL-2002; 2002US-00195835.

PA (CORI-) CORIXA CORP.

PI Gaiger A., Cheever MA;

PS WPI; 2004-070542/07.

PT Inducing an immune response in an animal, useful for treating or

PT preventing cancer, comprises administering a composition comprising a

PT viral vector comprising an immunogenic portion of a WT1 polynucleotide.

XX Example 1; SEQ ID NO 3; 229pp; English.

XX The invention relates to a novel method for inducing an immune response

XX in an animal which involves administering a first and a second

XX composition comprising a first and a second viral vector, respectively,

XX each having at least an immunogenic portion of a WT1 (Wilm's tumour)

XX polynucleotide operably linked to an expression control sequence. The

XX method of the invention has immunostimulant and cytostatic applications

XX and may be useful for generating or enhancing an immune response to WT1,

XX possibly via the production of a vaccine, as well as for preventing

XX and/or treating malignant diseases such as leukaemia and cancer. The

XX current sequence is that of the murine WT1 immunogenic peptide of the

XX invention.

Query Match 100.0%; Score 123; DB 8; Length 23;

Best Local Similarity 100.0%; Pred. No. 1.4e-12;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Oy      1 PSQSSGQARMFPNAPYLPSCLE 23
        |||||||
Cc      1 PSQSSGQARMFPNAPYLPSCLE 23
Db

RESULT 15
ID      ADL57246 standard; peptide; 23 AA.
AC      ADL57246;
XX
DT      20-MAY-2004 (first entry)
XX
DE      Mouse Wlms' tumour, WT-1, immunogenic peptide #1.
XX
KW      Mouse; Wlms' tumour; WT1; cancer; cytostatic; immunogen; antigen;
KW      vaccine; T-cell; MHC; Major Histocompatibility Complex; HLA-A2;
KW      human leukocyte antigen; Ral2; HIS tag; twin arginine translocator; TAT;
KW      malignant disease.
XX
OS      Mus musculus.
XX
PN      US2003215458-A1.
XX
PD      20-NOV-2003.
XX
PF      30-OCT-2002; 2002US-00286333.
XX
PR      30-SEP-1998; 98US-00164223.
PR      25-MAR-1999; 99US-00276484.
PR      06-OCT-2000; 2000US-00684361.
PR      09-OCT-2000; 2000US-00685830.
PR      15-FEB-2001; 2001US-00785019.
PR      24-AUG-2001; 2001US-00938864.
PR      30-OCT-2001; 2001US-00002603.
PR      16-APR-2002; 2002US-00125635.
PR      12-JUL-2002; 2002US-00195835.
PR      16-SEP-2002; 2002US-00244830.
XX
PA      (CORI-) CORIXA CORP.
XX
PI      Gaiger A, Mcneill PD, Jaya N;
XX
DR      WPI; 2004-021827/02.
XX
PT      New polypeptides and polynucleotides useful for generating or enhancing
PT      an immune response to Wlms' tumor, or for treating and/or preventing
PT      malignant diseases, e.g. cancer.
XX
PS      Example 1; SEQ ID NO 3; 259pp; English.
XX
Cc      The invention relates to an isolated polypeptide comprising an
Cc      immunogenic portion of a Wlms' tumour antigen (WT1), or their variants
Cc      that differs in substitution(s), deletion(s), addition(s) and/or
Cc      insertion(s), where ability of the variant to react with WT1-specific
Cc      antisera and/or T-cell lines or clones is not substantially diminished.
Cc      Also included are a fusion protein comprising at least one WT1
Cc      polypeptide, an isolated polynucleotide encoding the fusion protein, a
Cc      composition comprising a WT1 polypeptide in combination with a
Cc      pharmaceutical carrier or excipient, a vaccine comprising a WT1
Cc      polypeptide in combination with a non-specific immune response enhancer,
Cc      an expression vector comprising the polynucleotide operably linked to an
Cc      expression control sequence and a host cell transformed or transfected
Cc      with the expression vector. The immunogenic portion of the WT1
Cc      polypeptide has been modified such that the ability of the immunogenic
Cc      portion to bind to an MHC (Major Histocompatibility Complex) molecule or
Cc      to HLA-A2 is increased relative to that of the immunogenic portion. The
Cc      WT1 polypeptide may comprise a Wlms' tumour antigen having a deletion of
Cc      a proline rich region at amino acid positions 54-58 of the Wlms' tumour
Cc      antigen. The fusion partner is selected from Ral2, protein D, LYTA, a HIS
Cc      tag, a targeting signal capable of directing a polypeptide to the
Cc      endosomal/lysosomal compartment, twin arginine translocator (TAT), and
Cc      truncated twin arginine translocator. The polypeptide, polynucleotide or

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Cc      compositions comprising them may be used for generating or enhancing an
Cc      immune response to Wlms' tumour, and for treating and/or preventing
Cc      malignant diseases, e.g. cancer. The compositions may be used as markers
Cc      for the progression of cancer. The present sequence is a mouse WT1
Cc      polypeptide immunogenic peptide.
XX
SQ      Sequence 23 AA;

```

```

Query Match      100.0%; Score 123; DB 8; Length 23;
Best Local Similarity 100.0%; Pred. NO.1.4e-12;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy      1 PSQSSGQARMFPNAPYLPSCLE 23
        |||||||
Cc      1 PSQSSGQARMFPNAPYLPSCLE 23
Db

```

```

Search completed: November 23, 2005, 05:12:34
Job time : 190 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 23, 2005, 05:05:29 ; Search time 38 Seconds
(without alignments)
58.236 Million cell updates/sec

Title: US-09-164-223-2

Perfect score: 123
Sequence: 1 PSQASSGQARMFPNAPLPSCLE 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	123	100.0	448	2	S33926 Wilms' tumor prote
2	123	100.0	449	2	A38080 Wilms' tumor suscep
3	123	100.0	449	2	A39692 Wilms' tumor prote
4	103	83.7	410	2	UC5046 Wilms' tumor suppr
5	52	42.3	82	2	S02660 9K protein (clone
6	49	39.8	634	2	E82999 probable beta-keto
7	48	39.8	885	2	S61189 probable membrane
8	48	39.0	188	2	JU0451 hypothetical 21K p
9	48	39.0	188	2	IS9116 myc protein - huma
10	48	39.0	188	2	A29867 hypothetical 20K p
11	48	39.0	188	2	I79500 myc protein - huma
12	48	39.0	600	2	D83286 hypothetical prote
13	48	39.0	618	2	S68450 zinc apoptosis inhibito
14	48	39.0	778	2	T17679 proline-rich prote
15	48	38.2	271	2	UC4584 insulin-like growt
16	47	38.2	271	2	I48604 insulin-like growt
17	47	38.2	271	2	JC1463 insulin-like growt
18	47	38.2	272	2	A53748 insulin-like growt
19	47	38.2	815	2	B30843 glutenin high mole
20	47	38.2	815	2	JN0689 glutenin, high-mol
21	47	38.2	830	2	S15720 glutenin high mole
22	46	37.4	545	2	I36123 probable lyso1-trN
23	46	37.4	606	2	I45560 NADH2 dehydrogenas
24	46	37.4	955	2	T00247 zinc finger protei
25	45.5	37.0	704	2	T24517 hypothetical prote
26	45	36.6	381	2	A54415 transcription fact
27	45	36.6	382	2	A48492 polyantharide exp
28	45	36.6	484	2	UC7350 N-acetylglucosamin
29	45	36.6	488	2	T33739 hypothetical prote

30	44	35.8	292	2	G64695 conserved hypothet
31	44	35.8	292	2	A71824 probable ribonucle
32	44	35.8	376	2	T45097 hypothetical prote
33	44	35.8	393	2	T20268 hypothetical prote
34	44	35.8	449	2	UC5117 translation elonga
35	44	35.8	472	2	T04855 hypothetical prote
36	44	35.8	590	2	T11098 NADH2 dehydrogenas
37	44	35.8	602	2	S47880 NADH2 dehydrogenas
38	44	35.8	615	2	A82025 probable outer mem
39	44	35.8	726	2	S67044 NF1 protein - yea
40	44	35.8	738	1	TFHDM melanotransferrin
41	44	35.8	1286	2	B71413 hypothetical prote
42	43.5	35.4	188	2	A39787 teratocarcinoma-de
43	43.5	35.4	188	2	A30362 teratocarcinoma-de
44	43.5	35.4	337	1	UT0286 glyceraldehyde-3-P
45	43.5	35.4	832	2	S67505 DNA-directed DNA p

ALIGNMENTS

RESULT 1
S33926
Wilms' tumor protein WT1 - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 10-May-1996
C/Accession: S33926
R/Sharma, P.M.; Yang, X.; Bowman, M.; Roberts, V.; Sukumar, S.
A/Title: Molecular cloning of rat Wilms' tumor complementary DNA and a study of messeng
A/Reference number: S33926, PMID:93046155, PMID:1330293
A/Accession: S33926
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-448 <SHA>
A/Cross-references: UNIPARC:UPI000017CA1C, EMBL:X69716
C/Genetics:
A/Gene: WT1
C/Keywords: tumor suppressor

Query Match 100.0%; Score 123; DB 2; Length 448;
Best Local Similarity 100.0%; Pred. No. 4, 2e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQASSGQARMFPNAPLPSCLE 23
Db 116 PSQASSGQARMFPNAPLPSCLE 138

RESULT 2

A38080
Wilms tumor susceptibility protein WT1 - human
C/Species: Homo sapiens (man)
C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 20-Jun-2000
C/Accession: A38080, S08273, A34673, I38504, I52811, I58315, A56411, S26286

R/Gesseler, M.; Konig, A.; Bruns, G.A.
Genomics 12, 807-813, 1992
A/Title: The genomic organization and expression of the WT1 gene.
A/Reference number: A38080, PMID:92241883, PMID:1572653

A/Accession: A38080
A/Molecule type: DNA
A/Residues: 1-449 <GES1>
A/Cross-references: UNIPARC:UPI000017C420, GB:X61631, GB:S99414, NID:G37981, PIND:CAA431
A/Note: It is uncertain whether Met-1 is the initiator or whether translation is initia
A/Note: the sequence in GenBank entry HSWTGEEX1, release 113.0, PIND:CAA43819.1 differs
A/Gesseler, M.; Pouscka, A.; Cavenee, W.; Nerve, R.L.; Orkin, S.H.; Bruns, G.A.P.

Nature 343, 774-778, 1990
A/Title: Homozygous deletion in Wilms tumours of a zinc-finger gene identified by chrom
A/Reference number: S08273, PMID:90158822, PMID:2154702
A/Accession: S08273
A/Molecule type: mRNA

A/Residues: SRQRPQALNPPTACPLPHRPPSLPTHTPPRAGTAAQAPGRRLAAILDFLLQDPASTCVPEPASQH
hypothetical prote

A:Cross-references: UNIPARC:UPI000016B316; EMBL:X51630; NID:g37977; PIDN:CAA35956.1; PID:R:Call, K.M.; Glaeser, T.; Ito, C.Y.; Buckler, A.J.; Pelletier, J.; Haber, D.A.; Rose, E. Cell 60, 509-520, 1990
 A:Title: Isolation and characterization of a zinc finger polypeptide gene at the human C:Accession: A34673; MUID:90150277; PMID:2154335
 A:Residues: 85-249, 267-364, 'F', 366-386, 'T', 388-407, 411-449 <CAL>
 A:Cross-references: UNIPARC:UPI000047983; GB:M30393; NID:g340381; PIDN:AAA36810.1; PID:R:Haber, D.A.; Sohn, R.L.; Buckler, A.J.; Pelletier, J.; Call, K.M.; Housman, D.E. Proc. Natl. Acad. Sci. U.S.A. 88, 9618-9622, 1991
 A:Title: Alternative splicing and genomic structure of the Wilms tumor gene WT1.
 A:Reference number: A56411; MUID:92052142; PMID:1658787
 A:Contents: annotation; alternative splicing
 R:Phelan, S.A.; Lindberg, C.; Call, K.M.
 Cell Growth Differ. 5, 677-686, 1994
 A:Title: Wilms' tumor gene, WT1, mRNA is down-regulated during induction of erythroid at A:Reference number: 138504; MUID:94368704; PMID:8086342
 A:Accession: 138504
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-18 <PHE>
 A:Cross-references: UNIPARC:UPI00000052B; EMBL:U06486; NID:g473563; PIDN:AAA62865.1; PID:R:Peletier, J.; Bruehling, W.; Kashan, C.E.; Maurer, S.M.; Manivel, J.C.; Striegel, J.E. Cell 67, 437-447, 1991
 A:Title: Germ-line mutations in the Wilms' tumor suppressor gene are associated with abno A:Reference number: 152811; MUID:92005721; PMID:1655284
 A:Accession: 152811
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 355-365, 'H', 367-377 <PEL>
 A:Cross-references: UNIPARC:UPI000011DDFA; GB:S61513; NID:g237599; PIDN:AAB20109.1; PID:A:Note: mutant form
 R:Hamilton, T.B.; Barilla, K.C.; Romanuk, P.J. Nucleic Acids Res. 23, 277-284, 1995
 A:Title: High affinity binding sites for the Wilms' tumour suppressor protein WT1.
 A:Reference number: 158315; MUID:95166649; PMID:7862533
 A:Accession: 158315
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 'MGHHHHHHHSSGHIEGRHM', 301-364, 'F', 366-386, 'T', 388-407, 411-449 <HAM>
 A:Cross-references: UNIPARC:UPI0000072BDE; GB:S75264; NID:g896246; PIDN:AAB33443.1; PID:A:Note: this sequence is engineered
 C:Genetics:
 A:Gene: GDB:WT1
 A:Cross-references: GDB:120496; OMIM:194070
 A:Map position: 11p13-11p13
 A:Introns: 148/1; 189/1; 223/2; 249/2; 266/2; 298/3; 349/1; 379/1; 410/1
 A:Note: mRNA transcripts containing both alternatively spliced regions are the most abundant
 C:Keywords: alternative splicing; DNA binding; kidney; tumor suppressor; zinc finger
 F:1-407/Product: Wilms tumor susceptibility protein WT1, splice form 1 #status predicted
 F:1-407, 411-449/Product: Wilms tumor susceptibility protein WT1, splice form 4 #status F
 F:1-249, 267-449/Product: Wilms tumor susceptibility protein WT1, splice form 3 #status F
 F:1-249, 267-407, 411-449/Product: Wilms tumor susceptibility protein WT1, splice form 2 #

Query Match 100.0%; Score 123; DB 2; Length 449;
 Best Local Similarity 100.0%; Pred. No. 4, 3e-11;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSQASSGQARMPNAPYLPSCLE 23
 |||||:|||||
 Db 117 PSQASSGQARMPNAPYLPSCLE 139

RESULT 3
 A39692
 Wilms' tumor protein analog, WT1 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 16-Feb-1997
 C:Accession: A39692
 R:Buckler, A.J.; Pelletier, J.; Haber, D.A.; Glaeser, T.; Housman, D.E. Mol. Cell. Biol. 11, 1707-1712, 1991
 A:Title: Isolation, characterization, and expression of the murine Wilms' tumor gene (WT

A:Reference number: A39692; MUID:91141522; PMID:1671709
 A:Accession: A39692
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-449 <BUC>
 A:Cross-references: UNIPARC:UPI0000147984; GB:M55512
 C:Keywords: alternative splicing; DNA binding; transcription regulation; tumor suppressor

Query Match 100.0%; Score 123; DB 2; Length 449;
 Best Local Similarity 100.0%; Pred. No. 4, 3e-11;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSQASSGQARMPNAPYLPSCLE 23
 |||||:|||||
 Db 117 PSQASSGQARMPNAPYLPSCLE 139

RESULT 4
 JC5046
 Wilms' tumor suppressor protein - African clawed frog
 N:Alternate names: WT1
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 09-Jul-2004
 C:Accession: JC5046
 R:Semba, K.; Saito-Ueno, R.; Takayama, G.; Kondo, M. Gene 175, 167-172, 1996
 A:Title: cDNA cloning and its promoter-specific expression of the Wilms' tumor suppressor protein WT1
 A:Reference number: JC5046; MUID:97074667; PMID:8917094
 A:Contents: testis
 A:Accession: JC5046
 A:Molecule type: mRNA
 A:Residues: 1-410 <SEM>
 A:Cross-references: UNIPROT:P79958; UNIPARC:UPI000017BPA3; DDBJ:D82051
 C:Comment: This protein is involved in kidney morphogenesis.
 C:Genetics:
 A:Gene: wt1

Query Match 83.7%; Score 103; DB 2; Length 410;
 Best Local Similarity 78.3%; Pred. No. 4, 6e-08;
 Matches 18; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PSQASSGQARMPNAPYLPSCLE 23
 |||||:|||||
 Db 98 PSQATTGQARMPNAPYLPSCLE 120

RESULT 5
 S02660
 9K protein (clone pG4) - human
 C:Species: Homo sapiens (man)
 C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
 C:Accession: S02660
 R:Flammers, R.; Gross, G.; Mayr, U.; Collins, J. Eur. J. Biochem. 178, 93-99, 1988
 A:Title: Alternative mechanisms for gene activation induced by poly(I) * poly(UC) and N
 A:Reference number: S02660; MUID:89078418; PMID:3203696
 A:Accession: S02660
 A:Molecule type: mRNA
 A:Residues: 1-82 <LAM>
 A:Cross-references: UNIPROT:P13994; UNIPARC:UPI0000124FA8; EMBL:X13956; NID:g32574; PIDN

Query Match 42.3%; Score 52; DB 2; Length 82;
 Best Local Similarity 47.8%; Pred. No. 0, 5e-1;
 Matches 11; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Qy 1 PSQASSGQARMPNAPYLPSCLE 23
 |||||:|||||
 Db 23 PLEASSTRARVFPCLPLVACPE 45

RESULT 6
 B82999
 probable beta-ketocacyl synthase PA5174 [imported] - Pseudomonas aeruginosa (strain PAO1)

C/Species: *Pseudomonas aeruginosa*
 C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
 C/Accession: E82999
 R/Storer, C.K.; Pham, X.O.; Ewitt, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Linn, J.; Loty, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A/Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen
 A/Reference number: A82950; PMID:20437337; PMID:10984043
 A/Accession: E82999
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-634 <STO>
 A/Cross-references: UNIPROT:Q9HUI5; UNIPARC:UPI000006CF37; GB:AE004930; GB:AE004091; NID:A/Experimental source: strain PA01
 C/Genetics:
 A/Genes: PA5174

Query Match 39.8%; Score 49; DB 2; Length 634;
 Best Local Similarity 47.8%; Pred. No. 14;
 Matches 11; Conservative 3; Mismatches 5; Indels 4; Gaps 1;

QY 5 SSGQARMF---PNAPYLPSCLE 23
 DB 296 TSGQARVIVGNSEAPLPSCIE 318

RESULT 7

S61189
 Probable membrane protein YDR303c - Yeast (*Saccharomyces cerevisiae*)

N/Alternate names: hypothetical protein D9740.13
 C/Species: *Saccharomyces cerevisiae*

C/Date: 23-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 05-Oct-2004
 C/Accession: S61189

R/Ding, H.

submitted to the EMBL Data Library, June 1995

A/Description: The sequence of S. cerevisiae cosmid 9740.

A/Reference number: S61160

A/Accession: S61189

A/Molecule type: DNA

A/Residues: 1-885 <DIN>

A/Cross-references: UNIPROT:Q06639; UNIPARC:UPI0000053005; EMBL:U28374; NID:9849207; PID

C/Genetics:

A/Genes: SGD:RSC3; MIPS:YDR303c

A/Cross-references: SGD:S0002711

A/Map position: 4R

C/Keywords: transmembrane protein

F/9-47/Domain: GAL4 zinc binuclear cluster homology <GAL4>

F/42-438/Domain: transmembrane #status predicted <TM>

F/699-715/Domain: transmembrane #status predicted <TM2>

Query Match 39.8%; Score 49; DB 2; Length 885;

Best Local Similarity 50.0%; Pred. No. 20;
 Matches 10; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 PSQASSGQARMFPNAPYLP 20
 DB 53 PSSSSSSSTQVANGPYLNS 72

RESULT 8

JU0451
 hypothetical 21K protein (c-myc 5' region) - chimpanzee

C/Species: Pan troglodytes (chimpanzee)

C/Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
 C/Accession: JU0451

R/Aggaut, C.; Rigolec, M.; Eladadi, M.E.; Galibert, F.

Gene 97, 231-237, 1991

A/Title: Cloning and nucleotide sequence of the chimpanzee c-myc gene.

A/Reference number: JU0449; MUID:91153652; PMID:1999286

A/Accession: JU0451

A/Status: translation not shown

A/Molecule type: DNA

A/Residues: 1-188 <ARG>
 A/Cross-references: UNIPROT:Q95KX3; UNIPARC:UPI000006D15D; GB:M38057; NID:g176652; PIDN

Query Match 39.0%; Score 48; DB 2; Length 188;

Best Local Similarity 72.7%; Pred. No. 5.6;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 13 PNAPYLPSCLE 23
 DB 22 PGRPWLPSCLE 32

RESULT 9

I59116
 myc protein - human

C/Species: Homo sapiens (man)

C/Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 09-Jul-2004
 C/Accession: I59116

R/Finner, S.N.; Nishikura, K.; Finger, L.R.; Haluska, F.G.; Finan, J.; Nowell, P.C.; Ch

Proc. Natl. Acad. Sci. U.S.A. 85, 3052-3056, 1988

A/Title: Sequence analysis of the MYC oncogene involved in the t(8;14)(q24;q11) chromos

A/Reference number: I59116; MUID:88203638; PMID:2834731

A/Accession: I59116

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-188 <RES>

A/Cross-references: UNIPROT:Q14901; UNIPARC:UPI000006E838; GB:M20605; NID:g188974; PIDN

Query Match 39.0%; Score 48; DB 2; Length 188;

Best Local Similarity 72.7%; Pred. No. 5.6;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 13 PNAPYLPSCLE 23
 DB 22 PGRPWLPSCLE 32

RESULT 10

A29867
 hypothetical 20K protein (myc 5' region) (Burkitt lymphoma) - human

C/Species: Homo sapiens (man)

C/Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
 C/Accession: A29867

R/Shaw, D.C.; Moore, R.C.A.; Erikson, J.; Croce, C.M.

Proc. Natl. Acad. Sci. U.S.A. 84, 2824-2828, 1987

A/Title: MYC oncogene involved in a t(8;22) chromosome translocation is not altered in

A/Reference number: A29867; MUID:87204220; PMID:3033665

A/Accession: A29867

A/Molecule type: DNA

A/Residues: 1-188 <SHO>

A/Cross-references: UNIPROT:Q16591; UNIPROT:Q14901; UNIPARC:UPI0000179710

Query Match 39.0%; Score 48; DB 2; Length 188;

Best Local Similarity 72.7%; Pred. No. 5.6;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 13 PNAPYLPSCLE 23
 DB 22 PGRPWLPSCLE 32

RESULT 11

I79500
 myc protein - human

C/Species: Homo sapiens (man)

C/Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 09-Jul-2004
 C/Accession: I79500

R/Finner, S.N.; Nishikura, K.; Finger, L.R.; Haluska, F.G.; Finan, J.; Nowell, P.C.; Ch

Proc. Natl. Acad. Sci. U.S.A. 85, 3052-3056, 1988

A/Title: Sequence analysis of the MYC oncogene involved in the t(8;14)(q24;q11) chromos

A/Reference number: I59116; MUID:88203638; PMID:2834731

A/Accession: I79500

A/Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
 A:Residues: 1-188 <R8>
 A:Cross-references: UNIPROT:Q16591, UNIPARC:UPI000006D15D, GB:J03253, NID:g188976, PIDN:

Query Match 39.0%; Score 48; DB 2; Length 188;
 Best Local Similarity 72.7%; Pred. No. 5.6;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 13 PNAPYLPSCLE 23
 DB 22 PGRPWLPSCLE 32

RESULT 12

D83286
 hypochelical protein PA2886 [imported] - Pseudomonas aeruginosa (strain PA01)
 C:Species: Pseudomonas aeruginosa
 C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
 C:Accession: D83286

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Marrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Lim, J.; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
 A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: D83286
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-600 <STC>
 A:Cross-references: UNIPROT:Q9H2M1, UNIPARC:UPI00000C5861, GB:AE004714, GB:AE004091, NID:AE004091
 A:Experimental source: strain PA01
 A:Genetic8:
 A:Gene: PA2886

Query Match 39.0%; Score 48; DB 2; Length 600;
 Best Local Similarity 47.4%; Pred. No. 19;
 Matches 9; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 4 ASSGOARMPNAPYLPSCLE 22
 DB 125 AKSGIREMFSDAPFPMPVCV 143

RESULT 13

S68450
 apoptosis inhibitor hiap-2 - human
 C:Species: Homo sapiens (man)
 C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
 C:Accession: S68450

R:Litton, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farahani, Nature 379, 349-353, 1996
 A:Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of IAPs
 A:Reference number: A58182; MUID:96149249; PMID:8552191

A:Accession: S68450
 A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA
 A:Residues: 1-618 <LIS>
 A:Cross-references: UNIPROT:Q13490, UNIPARC:UPI000004A35C, EMBL:U45879, NID:g1184317, PI:U45879
 C:Function:
 A:Description: apoptotic suppressor
 C:Keywords: apoptosis; zinc finger
 F:567-611/Domain: RING finger homology <RNG>

Query Match 39.0%; Score 48; DB 2; Length 618;
 Best Local Similarity 50.0%; Pred. No. 20;
 Matches 10; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 4 ASSGOARMPNAPYLPSCLE 23
 DB 236 AMSEHRRFPNCPLENSLE 255

RESULT 14

T17679
 proline-rich protein A189R - Chlorella virus PBCV-1
 C:Species: Chlorella virus PBCV-1
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T17679

R:Graves, M.V.; Van Etten, J.L.
 submitted to the EMBL Data Library, May 1999
 A:Reference number: Z18806

A:Accession: T17679
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-778 <GRA>
 A:Cross-references: UNIPROT:Q84509, UNIPARC:UPI00000E8F2, EMBL:U42580, NID:g4028896, PI:U42580
 A:Experimental source: specific host Chlorella strain NC64A
 A:Genetic8:
 A>Note: A189R

Query Match 39.0%; Score 48; DB 2; Length 778;
 Best Local Similarity 47.1%; Pred. No. 25;
 Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 PQASGOARMPNAPY 17
 DB 170 PQASGSAGLFXKRP 186

RESULT 15

UC4584
 insulin-like growth factor binding protein-5 precursor - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C>Date: 10-Apr-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
 C:Accession: UC4584; G23734

R:White, M.E.; Disco, R.; Hathaway, M.R.; Mickelson, J.; Dayton, W.R.
 Biochem. Biophys. Res. Commun. 218, 248-253, 1996

A:Title: Molecular cloning and sequence analysis of the porcine insulin-like growth factor binding protein-5
 A:Reference number: UC4584; MUID:96136309; PMID:8573141

A:Accession: UC4584
 A:Molecule type: mRNA

A:Residues: 1-271 <WHI>
 A:Cross-references: UNIPROT:Q28985, UNIPARC:UPI000012D1E, GB:U41340, NID:g1173906, PIDN:U41340
 A:Experimental source: skeletal muscle
 R:Shimada, S.; Gao, L.; Shimada, M.; Ling, N.
 Mol. Endocrinol. 5, 938-948, 1991

A:Title: Isolation and molecular cloning of insulin-like growth factor-binding protein-6
 A:Reference number: A23734; MUID:92049376; PMID:1719383

A:Accession: G23734
 A:Molecule type: protein

A:Residues: 20-25, 'X', 27-28, 'X', 30-36, 'X', 38-39 <SHI>
 A:Cross-references: UNIPARC:UPI00000866D5

C:Comment: This protein has essential roles in the regulation and coordination of insulin-like growth factor production and differentiation, and is important in the growth of the developing fetus.
 C:Superfamily: insulin-like growth factor binding protein; thyroglobulin type I repeat
 C:Keywords: differentiation; skeletal muscle
 F:1-19/Domain: signal sequence; status predicted <SIG>
 F:20-27/Product: insulin-like growth factor binding protein-5; status experimental <MAT>
 F:191-262/Domain: thyroglobulin type I repeat homology <THY1>

Query Match 38.2%; Score 47; DB 2; Length 271;
 Best Local Similarity 47.4%; Pred. No. 12;
 Matches 9; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 3 QASGOARMPNAPYLPSCLE 21
 DB 200 QELKASPRMVPRAVYLPVC 218

Search completed: November 23, 2005, 05:17:15
 Job time : 40 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 23, 2005, 05:05:10 ; Search time 229 Seconds
(without alignments)

70.861 Million cell updates/sec

Title: US-09-164-223-2

Sequence: 123
1 PCSASSGQARMPNAPYLSCL 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	123	100.0	249	Q6P138_HUMAN	Q6P138 homo sapien
2	123	100.0	429	Q4VXV5_HUMAN	Q4VXV5 homo sapien
3	123	100.0	432	Q4VXV6_HUMAN	Q4VXV6 homo sapien
4	123	100.0	446	WT1_PAF	P49992 ratius norv
5	123	100.0	449	WT1_HUMAN	P19544 homo sapien
6	123	100.0	449	WT1_MOUSE	P22561 mus musculu
7	123	100.0	449	WT1_PIG	O62651 sus scrofa
8	103	83.7	407	P79558_XENLA	P79558 xenopus lae
9	102	82.9	390	Q42223_TRASC	Q42223 trachemys s
10	99	80.5	392	Q91030_CHICK	Q91030 gallus gall
11	99	80.5	414	Q918A1_CHICK	Q918A1 gallus gall
12	99	80.5	417	Q918A0_CHICK	Q918A0 gallus gall
13	95	77.2	409	Q91657_XENLA	Q91657 xenopus lae
14	85	69.1	426	Q9W611_CYNPY	Q9W611 cynops pyr
15	82	66.7	392	Q9IBF0_ANGUA	Q9IBF0 anguilla ja
16	73	59.3	386	Q90XX8_ONCMY	Q90XX8 oncorhynch
17	73	59.3	388	Q90XX7_ONCMY	Q90XX7 oncorhynch
18	73	59.3	417	Q90XX6_ONCMY	Q90XX6 oncorhynch
19	67	54.5	434	Q4S0X7_TETNG	Q4S0X7 tetraodon n
20	65	52.8	416	Q93433_FUGRU	Q93433 fugu rubrip
21	63	51.2	250	Q98S74_BRARE	Q98S74 brachydanio
22	63	51.2	419	Q9PU77_BRARE	Q9PU77 brachydanio
23	61	49.6	418	Q90XX4_ONCMY	Q90XX4 oncorhynch
24	61	49.6	418	Q90XX5_ONCMY	Q90XX5 oncorhynch
25	54	43.9	621	Q54M23_DICD1	Q54M23 dictyosteli
26	52	42.3	82	9RD_HUMAN	P13994 homo sapien
27	52	42.3	410	Q8JIR9_ORYLA	Q8JIR9 oryzias lat
28	51	41.5	1352	Q80U45_MOUSE	Q80U45 mus musculu
29	50.5	41.1	628	Q7S409_NEUCR	Q7S409 neurospora
30	50	40.7	342	Q6TRI9_CULOJ	Q6TRI9 culex quin
31	50	40.7	465	Q55X19_CRYNE	Q55X19 cryptococcu

32	50	40.7	465	2	Q5XME6_CRYNE	Q5XME6 cryptococcu
33	50	40.7	836	2	Q4WTS2_ASFPU	Q4WTS2 aspergillus
34	50	40.7	913	2	Q6PP28_XENLA	Q6PP28 xenopus lae
35	50	40.7	1320	2	Q7E2K6_ORYSA	Q7E2K6 oryza sativ
36	49	39.8	302	2	Q8J174_EMENI	Q8J174 emeritella
37	49	39.8	634	2	Q9HUI5_PSEAR	Q9HUI5 pseudomonas
38	49	39.8	649	2	Q5B8R8_EMENI	Q5B8R8 aspergillus
39	49	39.8	743	2	Q941L0_SECCB	Q941L0 secale cere
40	49	39.8	781	2	Q941K6_SECCB	Q941K6 secale cere
41	49	39.8	811	2	Q941J7_MHEAT	Q941J7 triticum ae
42	49	39.8	811	2	Q941L5_SECCB	Q941L5 secale cere
43	49	39.8	885	1	RSC3_YEAST	Q06639 saccharomyc
44	48.5	39.4	2401	2	Q7R2L4_GIALA	Q7R2L4 giardia lam
45	48.5	39.0	131	2	Q57NQ3_SALCH	Q57NQ3 salmoneella

ALIGNMENTS

RESULT 1	
Q6P138_HUMAN	
ID Q6P138_HUMAN PRELIMINARY;	PRT; 249 AA.
AC Q6P138;	
DT 05-JUL-2004 (TrEMBLrel. 27, Created)	
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)	
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)	
DE WT1 protein.	
GN Name=WT1;	
OS Homo sapiens (Human).	
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;	
OC Homo.	
OX NCBI_TaxID=9606;	
RN [1]	
RP NUCLEOTIDE SEQUENCE.	
RC TISSUE=Brain;	
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;	
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,	
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,	
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,	
RA Datchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,	
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,	
RA Brownstein M.J., Uedl T.B., Toshitsuki S., Carninci P., Prange C.,	
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhany S.J.,	
RA Bosak S.A., McKean P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	
RA Fahy J., Hellton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,	
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,	
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,	
RA Butterfield Y.S.N., Krzywinski M.I., Skalka U., Smalhus D.E.,	
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,	
RT "generation and initial analysis of more than 15,000 full-length human	
RL and mouse cDNA sequences."	
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).	
RP NUCLEOTIDE SEQUENCE.	
RC TISSUE=Brain;	
RG NIH MCC Project;	
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.	
DR EMBL; BC046461; AA046461.1; -, mRNA.	
DR GO; GO:0005634; C:nucleus; IEA.	
DR GO; GO:0003700; F:transcription factor activity; IEA.	
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.	
DR InterPro; IPR000976; Wilm_tumour.	
DR Pfam; Pf02165; WT1.1.	
DR PRINTS; PR00049; WILKSTUMOUR.	
SO SEQUENCE 249 AA; 25967 MW; 33F53B96A79CBF28 CRC64;	
Query Match	100.0%; Score 123; DB 2; Length 249;
Best Local Similarity	100.0%; Pred. No. 3; 5e-10;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PSQASSGQARMPNAPYLPSCLE 23
 |||||
 DB 117 PSQASSGQARMPNAPYLPSCLE 139

RESULT 2
 O4VXV5_HUMAN PRELIMINARY; PRT; 429 AA.
 AC O4VXV5;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Wilms tumor 1.
 GN Name=WT1; ORFNames=AL049692.1-001;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 OK NCBI_TaxId=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Frakland J.;
 RL Submitted (May-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL049692; CAI95759.1; -; Genomic_DNA.
 DR InterPro; IPR000976; Wilms_tumour.
 DR InterPro; IPR007087; Znf_C2H2.
 DR Pfam; PF02165; WT1; 1.
 DR Pfam; PF00096; zF-C2H2; 4.
 DR PRINTS; PR00049; WILMSTUMOUR.
 DR PRODOM; PD000003; znf_C2H2; 2.
 DR SMART; SM00355; Znf_C2H2; 4.
 SQ SEQUENCE 429 AA; 47195 MW; C2P9912E0A4DA3DB CRC64;

Query Match 100.0%; Score 123; DB 2; Length 429;
 Best Local Similarity 100.0%; Pred. No. 6.3e-10;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PSQASSGQARMPNAPYLPSCLE 23
 |||||
 DB 117 PSQASSGQARMPNAPYLPSCLE 139

RESULT 3
 O4VXV6_HUMAN PRELIMINARY; PRT; 432 AA.
 AC O4VXV6;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Wilms tumor 1.
 GN Name=WT1; ORFNames=AL049692.1-003;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 OK NCBI_TaxId=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Frakland J.;
 RL Submitted (May-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL049692; CAI95758.1; -; Genomic_DNA.
 DR InterPro; IPR000976; Wilms_tumour.
 DR InterPro; IPR007087; Znf_C2H2.
 DR Pfam; PF02165; WT1; 1.
 DR Pfam; PF00096; zF-C2H2; 4.
 DR PRINTS; PR00049; WILMSTUMOUR.
 DR PRODOM; PD000003; znf_C2H2; 2.
 DR SMART; SM00355; Znf_C2H2; 4.

DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
 DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 4.
 KM Metal-binding; Nuclear_protein; ZINC; Zinc-finger.
 SQ SEQUENCE 432 AA; 47511 MW; 1ACACB35630A92 CRC64;

Query Match 100.0%; Score 123; DB 2; Length 432;
 Best Local Similarity 100.0%; Pred. No. 6.3e-10;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PSQASSGQARMPNAPYLPSCLE 23
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 DB 117 PSQASSGQARMPNAPYLPSCLE 139

RESULT 4
 WT1_RAT STANDARD; PRT; 448 AA.
 ID WT1_RAT
 AC P49952;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Wilms' tumor protein homolog.
 GN Name=WT1; Synonyms=Wt-1;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Rattus.
 OK NCBI_TaxId=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE (ISOFORMS 1; 2; 3 AND 4).
 RC STRAIN=Sprague-Dawley; TISSUE=Kidney;
 RX MEDLINE=93046155; PubMed=1330293;
 RA Sharma P.M., Yang X., Bowman M., Roberts V., Sukumar S.;
 RT "Molecular cloning of rat Wilms' tumor complementary DNA and a study
 of messenger RNA expression in the urogenital system and the brain.";
 RL Cancer Res. 52:6407-6412(1992).
 CC -1- SIMILARITY: Potential role in transcriptional regulation. Recognizes
 and binds to the DNA sequence 5'-CGCCCCCGC-3'.
 CC -1- SUBUNIT: Interacts with ZNF224 via the zinc-finger region.
 CC -1- Interacts with WTAP (by similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=1;
 CC IsoId=P49952-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P49952-2; Sequence=VSP_006872, VSP_006873;
 CC Name=3;
 CC IsoId=P49952-3; Sequence=VSP_006872;
 CC Name=4;
 CC IsoId=P49952-4; Sequence=VSP_006873;
 CC -1- TISSUE SPECIFICITY: Kidney.
 CC -1- DEVELOPMENTAL STAGE: Expressed during kidney development.
 CC -1- SIMILARITY: Belongs to the EGR C2H2-type zinc-finger protein
 family.
 CC -1- SIMILARITY: Contains 4 C2H2-type zinc fingers.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; X69716; CAA49373.1; -; mRNA.
 CC DR HSSP; P08046; IFA1.
 CC DR TRANSFAC; T02352; -.
 CC DR ENSEMBL; ENSNRG00000013074; Rattus norvegicus.
 CC RGD; 3974; Wt1.
 CC InterPro; IPR000976; Wilms_tumour.
 CC InterPro; IPR007087; Znf_C2H2.
 CC Pfam; PF02165; WT1; 1.
 CC Pfam; PF00096; zF-C2H2; 4.
 CC PRINTS; PR00049; WILMSTUMOUR.

DR ProDom; P0000003; Znf_C2H2; 2.
 DR SMART; SM00355; Znf_C2H2; 4.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
 DR PROSITE; PS00157; ZINC_FINGER_C2H2_2; 4.
 KW Alternative splicing; Anti-oncogene; Cell cycle; DNA-binding;
 KW Metal-binding; Nuclear protein; Repeat; Transcription;
 KW Transcription regulation; Zinc; Zinc-finger.
 FT ZN_FING 322 346 C2H2-type 1.
 FT ZN_FING 352 376 C2H2-type 2.
 FT ZN_FING 382 404 C2H2-type 3.
 FT ZN_FING 413 437 C2H2-type 4.
 FT COMPEDAS 27 82 Pro-rich.
 FT VARSPLIC 249 265 Missing (in isoform 2 and isoform 3).
 FT VARSPLIC /FTId=VSP_006872.
 FT VARSPLIC /FTId=VSP_006873.
 FT VARSPLIC /FTId=VSP_006873.
 SO SEQUENCE 448 AA; 49193 MW; 329AC9AC1FF73F76 CRC64;
 Query Match 100.0%; Score 123; DB 1; Length 448;
 Best Local Similarity 100.0%; Pred. No. 6,6e-10;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PSQASSGQAMFPNAPYPSCLE 23
 DB 116 PSQASSGQAMFPNAPYPSCLE 138
 WT1_HUMAN STANDARD; PRT; 449 AA.
 ID P15544; Q15881; Q16256; Q16575; Q81Y25;
 AC WT1_HUMAN
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Wilm's tumor protein (WT1).
 GN Name=WT1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Fetal kidney;
 RX MEDLINE=9015882; PubMed=2154702; DOI=10.1038/343774a0;
 RA Geseler M., Poustka A., Cavenee W., Neye R.L., Ockin S.H.,
 RA Bruns G.A.P.;
 RT "Homozygous deletion in Wilms tumours of a zinc-finger gene identified
 RT by chromosome jumping.";
 RL Nature 343:774-778(1990).
 RN [2]
 RP NUCLEOTIDE SEQUENCE, AND ALTERNATIVE SPLICING.
 RC TISSUE=Placenta;
 RX MEDLINE=92052142; PubMed=1658787;
 RA Haber D.A., Sohn R.L., Buckler A.J., Pelletier J., Call K.M.,
 RA Housman D.E.;
 RT "Alternative splicing and genomic structure of the Wilms tumor gene
 RT WT1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:9618-9622(1991).
 RN [3]
 RP NUCLEOTIDE SEQUENCE (ISOFORM 4).
 RX MEDLINE=92241883; PubMed=1572653;
 RA Geseler M., Konig A., Bruns G.A.P.;
 RT "The genomic organization and expression of the WT1 gene.";
 RL Genomics 12:807-813(1992).
 RN [4]
 RP NUCLEOTIDE SEQUENCE (GENOMIC DNA).
 RA Rieder M.J., Livingston R.J., Daniels M.R., Chung M.-W.,
 RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Peol C.L., Robertson P.D.,
 RA Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
 RT "NIHES-SNPs, environmental genome project, NIHES ES1478, Department
 RT of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.

RN [5]
 RP NUCLEOTIDE SEQUENCE OF 85-449.
 RX MEDLINE=90150277; PubMed=2154335; DOI=10.1016/0092-8674(90)90601-A;
 RA Call K.M., Glaser T., Ito C.Y., Buckler A.J., Pelletier J.,
 RA Haber D.A., Rose E.A., Kral A., Veger H., Lewis W.H., Jones C.,
 RA Housman D.E.;
 RT "Isolation and characterization of a zinc finger polypeptide gene at
 RT the human chromosome 11 Wilms' tumor locus.";
 RL Cell 60:509-520(1990).
 RN [6]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RG Human chromosome 11 international sequencing consortium;
 RT Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 148-449 (ISOFORM 4).
 RC TISSUE=Testis;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnae.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haich F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Mullan S.J.,
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosa S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettaman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Whiting M., Madan A., Young A.C., Green E.D., Dickson M.C.,
 RA Blakeley R.W., Touchman J.W., Schmutz J., Myers R.M.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Skalska U., Smaluk D.E.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smaluk D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [8]
 RP NUCLEOTIDE SEQUENCE OF 301-449.
 RC TISSUE=Fetal kidney;
 RX MEDLINE=9516649; PubMed=7862533;
 RA Hamilton T.B., Barilla K.C., Romanuk P.J.;
 RT "High affinity binding sites for the Wilms' tumour suppressor protein
 RT WT1.";
 RL Nucleic Acids Res. 23:277-284(1995).
 RN [9]
 RP IDENTIFICATION OF START CODON, AND ALTERNATIVE SPLICE SITES.
 RX MEDLINE=91141522; PubMed=1671709;
 RA Buckler A.J., Pelletier J., Haber D.A., Glaser T., Housman D.E.;
 RT "Isolation, characterization, and expression of the murine Wilms'
 RT tumor gene (WT1) during kidney development.";
 RL Mol. Cell. Biol. 11:1707-1712(1991).
 RN [10]
 RP INTERACTION WITH WTAP.
 RX MEDLINE=20458888; PubMed=11001926;
 RA Little N.A., Hasle N.D., Davies R.C.;
 RT "Identification of WTAP, a novel Wilms' tumour 1-associated
 RT protein.";
 RL Hum. Mol. Genet. 9:2231-2239(2000).
 RN [11]
 RP INTERACTION WITH ZNF224.
 RX PubMed=1239212; DOI=10.1074/jbc.M205667200;
 RA Lee T.H., Liu S., Kim J., Pelletier J.;
 RT "Inhibition of Wilms tumor 1 transactivation by bone marrow zinc
 RT finger 2, a novel transcriptional repressor.";
 RL J. Biol. Chem. 277:44826-44837(2002).
 RN [12]
 RP REVIEW.
 RX MEDLINE=92207913; PubMed=1313285;
 RA Haber D.A., Buckler A.J.;
 RT "WT1: a novel tumor suppressor gene inactivated in Wilms' tumor.";
 RL New Biol. 4:97-106(1992).
 RN [13]

RP REVIEW.
 RX MEDLINE=93345769; PubMed=8393820;
 RA Rauber R.J. III;
 RT "The Wt1 Wilms tumor gene product: a developmentally regulated
 RT transcription factor in the kidney that functions as a tumor
 RT suppressor.";
 RL FASEB J. 7:896-903(1993).
 RN [14]
 RP VARIANT WT1 CYS-366.
 RX MEDLINE=92279213; PubMed=1317572;
 RA Little M.H., Prosser J., Condie A., Smith P.J., van Heyningen V.,
 RA Haefliger N.D.;
 RT "Zinc finger point mutations within the WT1 gene in Wilms tumor
 RT patients.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:4791-4795(1992).
 RN [15]
 RP VARIANTS DDS.
 RX MEDLINE=92005721; PubMed=1655284; DOI=10.1016/0092-8674(91)90194-4;
 RA Pelletier J., Bruening W., Kashtan C.E., Maurer S.M., Manivel J.C.,
 RA Striegel J.E., Houghton D.C., Junien C., Habib R., Fouser L.,
 RA Fine R.N., Silverman B.L., Haber D.A., Housman D.E.;
 RT "Germline mutations in the Wilms' tumor suppressor gene are associated
 RT with abnormal urogenital development in Denys-Drash syndrome.";
 RL Cell 67:437-447(1991).
 RN [16]
 RP VARIANTS DDS.
 RX MEDLINE=93265053; PubMed=1338906;
 RA Balld P.N., Santos A., Groves N., Jadesic L., Cowell J.K.;
 RT "Constitutional mutations in the WT1 gene in patients with Denys-Drash
 RT syndrome.";
 RL Hum. Mol. Genet. 1:301-305(1992).
 RN [17]
 RP NUCLEOTIDE SEQUENCE OF 385-405. AND VARIANT DDS TRP-394.
 RX MEDLINE=93250986; PubMed=1302008;
 RA Bruening W., Bardeesy N., Silverman B.L., Cohn R.A., Machin G.A.,
 RA Aronson A.J., Housman D., Pelletier J.;
 RT "Germline intronic and exonic mutations in the Wilms' tumour gene
 RT (WT1) affecting urogenital development.";
 RL Nat. Genet. 1:144-148(1992).
 RN [18]
 RP VARIANTS DDS.
 RX MEDLINE=93271983; PubMed=8388765;
 RA Little M.H., Williamson K.A., Mannens M., Kelsey A., Gosden C.,
 RA Haefliger N.D., van Heyningen V.;
 RT "Evidence that WT1 mutations in Denys-Drash syndrome patients may act
 RT in a dominant-negative fashion.";
 RL Hum. Mol. Genet. 2:259-264(1993).
 RN [19]
 RP VARIANTS DDS TRP-394 AND PRO-398.
 RX MEDLINE=94125627; PubMed=8295405;
 RA Tsuda M., Sakiyama T., Kitagawa T., Watanabe S., Watanabe T.,
 RA Takahashi S., Kawaguchi H., Ito K.;
 RT "Molecular analysis of two Japanese cases of Denys-Drash syndrome.";
 RL J. Inher. Metab. Dis. 16:876-880(1993).
 RN [20]
 RP VARIANT MESOTHELIOMA GLY-273.
 RX MEDLINE=94004972; PubMed=8401592;
 RA Park S., Schalling M., Bernard A., Maheswaran S., Shipley G.C.,
 RA Roberts D., Fletcher J., Shipman R., Rheinwald J., Demetri G.,
 RA Griffin J., Minden M., Housman D.E., Haber D.A.;
 RT "The Wilms tumour gene WT1 is expressed in murine mesoderm-derived
 RT tissues and mutated in a human mesothelioma.";
 RL Nat. Genet. 4:415-420(1993).
 RN [21]
 RP VARIANT DDS ARG-377.
 RX MEDLINE=94156335; PubMed=8112732; DOI=10.1007/BF00210593;
 RA Nordenskjold A., Friedman E., Anvret M.;
 RT "WT1 mutations in patients with Denys-Drash syndrome: a novel mutation
 RT in exon 8 and paternal allele origin.";
 RL Hum. Genet. 93:115-120(1994).
 RN [22]
 RP VARIANT DDS TYR-373.
 RX MEDLINE=97114281; PubMed=8956030;

RA Ghahremani M., Chan C.B., Bistritz T., Aladjem M.M., Tieder M.,
 RA Pelletier J.;
 RT "A novel mutation H373 in the Wilms' tumor suppressor gene, WT1,
 RT associated with Denys-Drash syndrome.";
 RL Hum. Hered. 46:336-338(1996).
 RN [23]
 RP VARIANTS WT1 SER-181 AND ALA-253.
 RX MEDLINE=97268681; PubMed=9108089; DOI=10.1073/pnas.94.8.3972;
 RA Schumacher V., Schneider S., Figue A., Wildhardt G., Harms D.,
 RA Schmidt D., Weirich A., Ludwig R., Royer-Pokora B.;
 RT "WT1 mutations in patients with Denys-Drash syndrome: a novel mutation
 RT in exon 8 and paternal allele origin.";
 RL Hum. Genet. 93:115-120(1994).
 RN [24]
 RP VARIANT DDS TRP-394 AND PRO-398.
 RX MEDLINE=94125627; PubMed=8295405;
 RA Tsuda M., Sakiyama T., Kitagawa T., Watanabe S., Watanabe T.,
 RA Takahashi S., Kawaguchi H., Ito K.;
 RT "Molecular analysis of two Japanese cases of Denys-Drash syndrome.";
 RL J. Inher. Metab. Dis. 16:876-880(1993).
 RN [25]
 RP VARIANT MESOTHELIOMA GLY-273.
 RX MEDLINE=94004972; PubMed=8401592;
 RA Park S., Schalling M., Bernard A., Maheswaran S., Shipley G.C.,
 RA Roberts D., Fletcher J., Shipman R., Rheinwald J., Demetri G.,
 RA Griffin J., Minden M., Housman D.E., Haber D.A.;
 RT "The Wilms tumour gene WT1 is expressed in murine mesoderm-derived
 RT tissues and mutated in a human mesothelioma.";
 RL Nat. Genet. 4:415-420(1993).
 RN [26]
 RP VARIANT DDS ARG-377.
 RX MEDLINE=94156335; PubMed=8112732; DOI=10.1007/BF00210593;
 RA Nordenskjold A., Friedman E., Anvret M.;
 RT "WT1 mutations in patients with Denys-Drash syndrome: a novel mutation
 RT in exon 8 and paternal allele origin.";
 RL Hum. Genet. 93:115-120(1994).
 RN [27]
 RP VARIANT DDS TYR-373.
 RX MEDLINE=97114281; PubMed=8956030;

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DR GO: GO:0005737, C:cytoplasm; IDA.
DR GO: GO:0005634, C:nucleus; IDA.
DR GO: GO:0005515, F:protein binding; IPI.
DR GO: GO:0030855, P:epithelial cell differentiation; IMP.
DR GO: GO:0001747, P:eye morphogenesis (sensu Mammalia); IMP.
DR GO: GO:0007281, P:germ cell development; IMP.
DR GO: GO:0009888, P:hirsutenesis; IMP.
DR GO: GO:0008584, P:male gonad development; IMP.
DR GO: GO:0001823, P:mesonephros development; IMP.
DR GO: GO:0001656, P:metanephros development; IMP.
DR GO: GO:0006357, P:regulation of transcription from RNA polyme. . .; IDA.
DR InterPro: IPR000976, Wilm's tumour.
DR InterPro: IPR007087, Znf_C2H2.
DR Pfam: PF02165, WT1.1.
DR PRINTS: PR00049, WILMSTUMOUR.
DR ProDom: PD000003, Znf_C2H2.2.
DR SMART: SM00355, Znf_C2H2.4.
DR PROSITE: PS00028, ZINC_FINGER_C2H2_1; 4.
DR PROSITE: PS0157, ZINC_FINGER_C2H2_2; 4.
DR Alternative splicing; Anti-oncogene; Cell cycle; DNA-binding;
KM Metal-binding; Nuclear protein; Repeat; Transcription;
KW Transcription regulation; Zinc; Zinc-finger.
FT ZN_FING 323 347 C2H2-type 1.
FT ZN_FING 353 377 C2H2-type 2.
FT ZN_FING 383 405 C2H2-type 3.
FT ZN_FING 414 438 C2H2-type 4.
FT COMPBIAS 28 83 Pro-rich.
FT VARSPIC 250 266 Missing (in isoform 2 and isoform 3).
FT VARSPIC 408 410 Missing (in isoform 2 and isoform 4).
FT VARSPIC 408 410 /FTId=VSP_006869.
SQ SEQUENCE 449 AA; 49246 MW; 962381E9C8D7A380 CRC64;

Query Match 100.0%; Score 123; DB 1; Length 449;
Best Local Similarity 100.0%; Pred. No. 6.6e-10;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQASSGQARMPNAPYLPSCLE 23
DB 117 PSQASSGQARMPNAPYLPSCLE 139

RESULT 7
WT1_PIG, STANDARD; PRT; 449 AA.
ID WT1_PIG
AC O62651;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Wilm's tumor protein homolog.
GN Name=WT1;
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sub.
NCBI_TaxID=9623;
[1]
RN NUCLEOTIDE SEQUENCE (ISOFORMS 1; 2; 3 AND 4).
RP STAIN=LMW; TISSUE=Kidney;
RX MEDLINE=96267201; PubMed=9602131; DOI=10.1016/S0378-1119(98)00112-7;
RA Teurturel N., Oda H., Nakatsuru Y., Imai Y., Zhang S., Ueno Y.,
RA Ishikawa T.;
RT "cDNA cloning and developmental expression of the porcine homologue of
WT1."
RL Gene 211:215-220(1998).
CC -1- FUNCTION: Potential role in transcriptional regulation. Recognizes
CC and binds to the DNA sequence 5'-CGCCCCGC-3'.
CC -1- SUBUNIT: Interacts with ZNF224 via the zinc-finger region.
CC Interacts with WTAP (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;

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CC CC Comment=Experimental confirmation may be lacking for some
CC isoforms;
CC Name=1;
CC IsoId=O62651-1; Sequence=Displayed;
CC Name=2;
CC IsoId=O62651-2; Sequence=VSP_006870, VSP_006871;
CC Name=3;
CC IsoId=O62651-3; Sequence=VSP_006870;
CC Name=4;
CC IsoId=O62651-4; Sequence=VSP_006871;
CC -1- DEVELOPMENTAL STAGE: Expressed during kidney development.
CC -1- SIMILARITY: Belongs to the EGR C2H2-type zinc-finger protein
CC family.
CC -1- SIMILARITY: Contains 4 C2H2-type zinc fingers.
CC -----
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CC -----
DR EMBL: AB010969; BAA28147.1; -; mRNA.
DR HSSP: P08046; 1P21.
DR InterPro: IPR000976; Wilm's tumour.
DR InterPro: IPR007087; Znf_C2H2.
DR Pfam: PF02165; WT1.1.
DR Pfam: PF00096; Zf_C2H2.4.
DR PRINTS: PR00049; WILMSTUMOUR.
DR ProDom: PD000003; Znf_C2H2.2.
DR SMART: SM00355; Znf_C2H2.4.
DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; 4.
DR PROSITE: PS0157; ZINC_FINGER_C2H2_2; 4.
DR Alternative splicing; Anti-oncogene; Cell cycle; DNA-binding;
KM Metal-binding; Nuclear protein; Repeat; Transcription;
KW Transcription regulation; Zinc; Zinc-finger.
FT ZN_FING 323 347 C2H2-type 1.
FT ZN_FING 353 377 C2H2-type 2.
FT ZN_FING 383 405 C2H2-type 3.
FT ZN_FING 414 438 C2H2-type 4.
FT COMPBIAS 28 83 Pro-rich.
FT VARSPIC 249 265 Missing (in isoform 2 and isoform 3).
FT VARSPIC 407 409 Missing (in isoform 2 and isoform 4).
FT VARSPIC 407 409 /FTId=VSP_006871.
SQ SEQUENCE 449 AA; 49166 MW; 9C3E557B96F5A7B3 CRC64;

Query Match 100.0%; Score 123; DB 1; Length 449;
Best Local Similarity 100.0%; Pred. No. 6.6e-10;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQASSGQARMPNAPYLPSCLE 23
DB 117 PSQASSGQARMPNAPYLPSCLE 139

RESULT 8
P79958_XENLA PRELIMINARY; PRT; 407 AA.
ID P79958;
AC P79958;
DT 01-MAY-1997 (Trembl,rel. 03, Created)
DT 01-MAY-1997 (Trembl,rel. 03, Last sequence update)
DT 01-OCT-2003 (Trembl,rel. 25, Last annotation update)
DE Wt1 protein.
GN Name=WT1;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodidae; Xenopus; Xenopus.
NCBI_TaxID=8155;
[1]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Testis;
RX MEDLINE=97074667; PubMed=8917094; DOI=10.1016/0378-1119(96)00143-6;

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RA  Semba K., Saito-Ueno R., Takayama G., Kondo M.;
RT  "cDNA cloning and its proneuro-specific expression of the Wilms'
RL  Gene 175:167-172(1996).
DR  EMBL; D82051; BAA11522.1; -, mRNA.
DR  PIR; JCS046; JCS046.
DR  HSSP; P08046; 1P47.
DR  GO; GO:0005634; C:nucleus; IEA.
DR  GO; GO:0046872; F:metal ion binding; IEA.
DR  GO; GO:0003676; F:nucleic acid binding; IEA.
DR  GO; GO:0003700; F:transcription factor activity; IEA.
DR  GO; GO:0008270; F:zinc ion binding; IEA.
DR  GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR  InterPro; IPR000976; Wilms tumour.
DR  InterPro; IPR007087; znf_C2H2.
DR  Pfam; PF02165; WTI; 1.
DR  Pfam; PF00096; zf_C2H2; 4.
DR  PRINTS; PR00049; WILMSTUMOUR.
DR  ProDom; PD000003; znf_C2H2; 2.
DR  SMART; SM00355; znf_C2H2; 4.
DR  PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
DR  PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.
DR  Metal-binding; Zinc; Zinc-finger.
SQ  SEQUENCE 407 AA; 45983 MW; E2554C658005870C CRC64;

Query Match
Best Local Similarity 83.7%; Score 103; DB 2; Length 407;
Matches 18; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY  1 PSQASSGQARMPNAPYLPSCLE 23
    |||::|||::|||::|||::|||
Db  98 PSQATTGQARMPNAPYLPSCLE 120

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RESULT 9
Q42223 TRASC PRELIMINARY; PRT; 390 AA.
AC 042223-
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Wilms tumor 1 protein.
GN Name=WT1;
OS Trachemys scripta (Red-eared slider turtle) (Pseudemys scripta).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Testudines; Cryptodira; Testudinoidae; Emydidae; Trachemyds.
OC NCBI_TaxId=34903;
[1]
RN NUCLEOTIDE SEQUENCE.
RP Spotila L.D., Hall S.E.;
RL Submitted (Aug-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF019779; AAB70832.1; -, mRNA.
DR HSSP; P08046; 1P47.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000976; Wilms tumour.
DR InterPro; IPR007087; znf_C2H2.
DR Pfam; PF02165; WTI; 1.
DR Pfam; PF00096; zf_C2H2; 3.
DR PRINTS; PR00049; WILMSTUMOUR.
DR ProDom; PD000003; znf_C2H2; 2.
DR SMART; SM00355; znf_C2H2; 4.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.
DR Metal-binding; Nuclear protein; Zinc; Zinc-finger.
SQ SEQUENCE 390 AA; 43620 MW; 1C9987435B927C2 CRC64;

Query Match
Best Local Similarity 82.9%; Score 102; DB 2; Length 390;
Matches 18; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

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Matches 18; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY  1 PSQASSGQARMPNAPYLPSCLE 23
    |||::|||::|||::|||::|||
Db  100 PTCQPSQARMPNAPYLPSCLE 122

RESULT 10
Q91030 CHICK PRELIMINARY; PRT; 392 AA.
AC Q91030-
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Chick Wilm's tumour protein (Fragment).
GN Name=CWT1;
OS Gallus gallus (chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxId=9031;
[1]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=whole embryo;
RX MEDLINE=96068905; PubMed=7478606;
RA Kent J., Coriat A.M., Sharpe P.T., Hastie N.D., van Heyningen V.;
RT "The evolution of WTI sequence and expression pattern in the
RT vertebrates."
RL Oncogene 11:1781-1792(1995).
[2]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=whole embryo;
RA Kent G.R.L.;
RL Submitted (Mar-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; X85731; CAAS9736.1; -, mRNA.
DR HSSP; Q60980; 1P7A.
DR SMR; Q91030; 318-384.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000976; Wilms tumour.
DR InterPro; IPR007087; znf_C2H2.
DR Pfam; PF02165; WTI; 1.
DR Pfam; PF00096; zf_C2H2; 3.
DR PRINTS; PR00049; WILMSTUMOUR.
DR ProDom; PD000003; znf_C2H2; 2.
DR SMART; SM00355; znf_C2H2; 3.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 3.
DR NON_TER 392
FT SEQUENCE 392 AA; 43869 MW; 761F01D350BAEDBF CRC64;

Query Match
Best Local Similarity 80.5%; Score 99; DB 2; Length 392;
Matches 18; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY  1 PSQASSGQARMPNAPYLPSCLE 23
    |||::|||::|||::|||::|||
Db  100 PSQPSGQARMPNAPYLPSCLE 122

RESULT 11
Q918A1 CHICK PRELIMINARY; PRT; 414 AA.
AC Q918A1-
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE WTI(-KTS) protein.
GN Name=WT1(-KTS);

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OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Ovary;
RA Kudo T.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB033633; BAA94793.1; -; mRNA.
DR HSP: P08046.1P47.
DR Ensembl: ENSGALG00000012115; Gallus gallus.
DR GO: GO:0005634; C:nucleus; IEA.
DR GO: GO:0046872; F:metal ion binding; IEA.
DR GO: GO:0003676; F:nucleic acid binding; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0008270; F:zinc ion binding; IEA.
DR GO: GO:0006355; P:regulation of transcription; DNA-dependent; IEA.
DR InterPro: IPR007087; Znf_C2H2.
DR Pfam: PF02165; WT1.1.
DR PRINTS: PR000049; WILMSTUMOUR.
DR ProDom: PD000003; Znf_C2H2; 2.
DR SMART: SM00355; Znf_C2H2; 4.
DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; 4.
DR PROSITE: PS0157; ZINC_FINGER_C2H2_2; 4.
KW Metal-binding; Nuclear protein; Zinc; Zinc-finger.
SQ SEQUENCE 414 AA; 46641 MW; 17EB22FB8428A2EF CRC64;

Query Match 80.5%; Score 99; DB 2; Length 414;
Best Local Similarity 78.3%; Pred. No. 2.5e-06;
Matches 18; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 PSQASSGQARMFPNAPYLPSCLE 23
Db 100 PSQPPSGQARMFPQRYLPNCLE 122

RESULT 12
Q918A0_CHICK
ID Q918A0_CHICK PRELIMINARY; PRT; 417 AA.
AC Q918A0;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE WT1(+KTS) protein.
GN Name=WT1(+KTS);
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Ovary;
RA Kudo T.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB033634; BAA94794.1; -; mRNA.
DR HSP: P08046.1P47.
DR Ensembl: ENSGALG00000012115; Gallus gallus.
DR GO: GO:0005634; C:nucleus; IEA.
DR GO: GO:0046872; F:metal ion binding; IEA.
DR GO: GO:0003676; F:nucleic acid binding; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0008270; F:zinc ion binding; IEA.
DR GO: GO:0006355; P:regulation of transcription; DNA-dependent; IEA.
DR InterPro: IPR007087; Znf_C2H2.
DR Pfam: PF02165; WT1.1.
DR PRINTS: PR000049; WILMSTUMOUR.

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DR ProDom: PD000003; Znf_C2H2; 2.
DR SMART: SM00355; Znf_C2H2; 4.
DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; 4.
DR PROSITE: PS0157; ZINC_FINGER_C2H2_2; 4.
KW Metal-binding; Nuclear protein; Zinc; Zinc-finger.
SQ SEQUENCE 417 AA; 46958 MW; 47BBF7F6448E7F6C CRC64;

Query Match 80.5%; Score 99; DB 2; Length 417;
Best Local Similarity 78.3%; Pred. No. 2.5e-06;
Matches 18; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 PSQASSGQARMFPNAPYLPSCLE 23
Db 100 PSQPPSGQARMFPQRYLPNCLE 122

RESULT 13
Q91657_XENLA
ID Q91657_XENLA PRELIMINARY; PRT; 409 AA.
AC Q91657;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE WT1.
GN Name=WT1;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE: 96363858; PubMed=8725280;
RX DOI=10.1002/(SICI)1097-0177(199606)206:2<131::AID-AJ23.3.CO;2-I;
RA Carroll T.J., Vize P.D.;
RT "Wt1s' tumor suppressor gene is involved in the development of
RT disparate kidney forms: evidence from expression in the Xenopus
RT pronephros."
RT Dev. Dyn. 206:131-138(1996).
DR EMBL: U42011; AAB53152.1; -; mRNA.
DR HSP: P08046.1P47.
DR GO: GO:0005634; C:nucleus; IEA.
DR GO: GO:0046872; F:metal ion binding; IEA.
DR GO: GO:0003676; F:nucleic acid binding; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0008270; F:zinc ion binding; IEA.
DR GO: GO:0006355; P:regulation of transcription; DNA-dependent; IEA.
DR InterPro: IPR007087; Znf_C2H2.
DR Pfam: PF02165; WT1.1.
DR PRINTS: PR000049; WILMSTUMOUR.
DR ProDom: PD000003; Znf_C2H2; 2.
DR SMART: SM00355; Znf_C2H2; 4.
DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; 4.
DR PROSITE: PS0157; ZINC_FINGER_C2H2_2; 4.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 409 AA; 46186 MW; 2217FC04612CDE10 CRC64;

Query Match 77.2%; Score 95; DB 2; Length 409;
Best Local Similarity 73.9%; Pred. No. 9.9e-06;
Matches 17; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 PSQASSGQARMFPNAPYLPSCLE 23
Db 97 PSQATTGQARMFPNAPYLPNCLE 119

RESULT 14
Q9M611_CYNPY
ID Q9M611_CYNPY PRELIMINARY; PRT; 426 AA.
AC Q9M611;
DT 01-NOV-1999 (Tremblrel. 12, Created)

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DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE WTI.
OS Cynops pyrrhogaster (Japanese common newt).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
OX NCBI_TaxID=8330;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RX MEDLINE=99081568; PubMed=9865970;
RA DOI=10.1046/j.1440-169x.1998.t01-4-00004.x;
RA Nakayama Y., Yamamoto T., Matsuda Y., Abe S.-I.;
RT "Cloning of cDNA for newt WTI and the differential expression during
RT spermatogenesis of the Japanese newt, Cynops pyrrhogaster.";
RL dev. Growth Differ. 40:599-608(1998).
DR EMBL; AB013888; BAA76399.1; -; mRNA.
DR HSSP; P08046; 1P47.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF02165; WTI; 1.
DR Pfam; PF00096; zf-C2H2; 4.
DR PRINTS; PR00049; WILMSTUMOUR.
DR ProDom; PD000003; Znf_C2H2; 2.
DR SMART; SM00355; Znf_C2H2; 4.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.
DR Metal-binding; Nuclear protein; Zinc; Zinc-finger.
SQ SEQUENCE 426 AA; 47591 MW; 46A0B158A9F79C6C CRC64;

Query Match 69.1%; Score 85; DB 2; Length 426;
Best Local Similarity 65.2%; Pred. No. 0.00033;
Matches 15; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 PSQASSGQARMPNAPYLPSCLE 23
DB 107 PSQPPAQVRFMSNGPYLPNCLE 129

RESULT 15
Q9IBF0 ANGJA PRELIMINARY; PRT; 392 AA.
ID Q9IBF0;
AC Q9IBF0;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Wtlns' tumor protein.
GN Name=EWT1;
OS Anguilla japonica (Japanese eel).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
OC Anguilla.
OX NCBI_TaxID=7937;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=20183666; PubMed=10717475; DOI=10.1016/S0378-1119(00)00016-0;
RA Nakatsuru Y., Minami K., Yoshikawa A., Zhu J.-J., Oda H., Masahito P.,
RA Okamoto N., Nakamura Y., Ishikawa T.;
RT "Eel WTI sequence and expression in spontaneous nephroblastomas in
RT Japanese eel.";
RL Gene 245:245-251(2000).
DR EMBL; AB030741; BAA90558.1; -; mRNA.
DR HSSP; P08046; 1P47.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.

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DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR007087; Wtlns tumour.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF02165; WTI; 1.
DR Pfam; PF00096; zf-C2H2; 4.
DR PRINTS; PR00049; WILMSTUMOUR.
DR ProDom; PD000003; Znf_C2H2; 3.
DR SMART; SM00355; Znf_C2H2; 4.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.
DR Metal-binding; Nuclear protein; Zinc; Zinc-finger.
SQ SEQUENCE 392 AA; 43892 MW; DAE1A4828F43DF6 CRC64;

Query Match 66.7%; Score 82; DB 2; Length 392;
Best Local Similarity 60.9%; Pred. No. 0.00086;
Matches 14; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 PSQASSGQARMPNAPYLPSCLE 23
DB 103 PSQPPGQARMPNAPYLPNCVD 125

Search completed: November 23, 2005, 05:16:30
Job time : 231 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 23, 2005, 05:16:36 ; Search time 160 Seconds
(Without alignments)
57.203 Million cell updates/sec

Title: US-09-164-223-2

Sequence: 1 PSQASSGQAMFPNAPYLPSCLE 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main.*
1: /cgn2_6/ptodaca/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodaca/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodaca/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodaca/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodaca/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodaca/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	123	100.0	23	US-09-938-864-2	Sequence 2, Appli
2	123	100.0	23	US-09-938-864-3	Sequence 3, Appli
3	123	100.0	23	US-09-938-864-4	Sequence 4, Appli
4	123	100.0	23	US-09-938-864-5	Sequence 5, Appli
5	123	100.0	23	US-09-938-864-6	Sequence 6, Appli
6	123	100.0	23	US-09-938-864-7	Sequence 7, Appli
7	123	100.0	23	US-09-938-864-8	Sequence 8, Appli
8	123	100.0	23	US-09-938-864-9	Sequence 9, Appli
9	123	100.0	23	US-09-938-864-10	Sequence 10, Appli
10	123	100.0	23	US-09-938-864-11	Sequence 11, Appli
11	123	100.0	23	US-09-938-864-12	Sequence 12, Appli
12	123	100.0	23	US-09-938-864-13	Sequence 13, Appli
13	123	100.0	23	US-09-938-864-14	Sequence 14, Appli
14	123	100.0	23	US-09-938-864-15	Sequence 15, Appli
15	123	100.0	23	US-09-938-864-16	Sequence 16, Appli
16	123	100.0	23	US-09-938-864-17	Sequence 17, Appli
17	123	100.0	23	US-09-938-864-18	Sequence 18, Appli
18	123	100.0	23	US-09-938-864-19	Sequence 19, Appli
19	123	100.0	23	US-09-938-864-20	Sequence 20, Appli
20	123	100.0	23	US-09-938-864-21	Sequence 21, Appli
21	123	100.0	23	US-09-938-864-22	Sequence 22, Appli
22	123	100.0	23	US-09-938-864-23	Sequence 23, Appli
23	123	100.0	23	US-09-938-864-24	Sequence 24, Appli
24	123	100.0	23	US-09-938-864-25	Sequence 25, Appli
25	123	100.0	23	US-09-938-864-26	Sequence 26, Appli
26	123	100.0	23	US-09-938-864-27	Sequence 27, Appli
27	123	100.0	23	US-09-938-864-28	Sequence 28, Appli

28	123	100.0	152	4	US-10-427-717-343	Sequence 343, App
29	123	100.0	152	4	US-10-427-717-343	Sequence 343, App
30	123	100.0	154	3	US-09-929-315-5	Sequence 5, Appli
31	123	100.0	154	3	US-09-929-315-5	Sequence 5, Appli
32	123	100.0	214	3	US-09-938-864-395	Sequence 395, App
33	123	100.0	214	4	US-10-125-635A-395	Sequence 395, App
34	123	100.0	214	4	US-10-002-603-395	Sequence 395, App
35	123	100.0	214	4	US-10-195-835-395	Sequence 395, App
36	123	100.0	214	4	US-10-286-333-395	Sequence 395, App
37	123	100.0	214	4	US-10-244-830-395	Sequence 395, App
38	123	100.0	214	4	US-10-427-717-395	Sequence 395, App
39	123	100.0	256	3	US-09-938-864-335	Sequence 335, App
40	123	100.0	256	3	US-10-125-635A-335	Sequence 335, App
41	123	100.0	256	4	US-10-125-635A-335	Sequence 335, App
42	123	100.0	256	4	US-10-002-603-335	Sequence 335, App
43	123	100.0	256	4	US-10-195-835-335	Sequence 335, App
44	123	100.0	256	4	US-10-286-333-335	Sequence 335, App
45	123	100.0	256	4	US-10-244-830-335	Sequence 335, App

ALIGNMENTS

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RESULT 1
US-09-938-864-2
; Sequence 2, Application US/09938864
; Publication No. US20030072767A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Moesman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydeton, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C5
; CURRENT APPLICATION NUMBER: US/09/938,864
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-938-864-2
Query Match          100.0%; Score 123; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 56-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PSQASSGQAMFPNAPYLPSCLE 23
Db 1 PSQASSGQAMFPNAPYLPSCLE 23
RESULT 2
US-09-938-864-3
; Sequence 3, Application US/09938864
; Publication No. US20030072767A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Moesman, Sally
; APPLICANT: Evans, Lawrence
```

```

; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C5
; CURRENT APPLICATION NUMBER: US/09/938,864
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-938-864-3

Query Match          100.0%; Score 123; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 5e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 PSQASSGQARMFPNAPYLPSCLE 23
DB      1 PSQASSGQARMFPNAPYLPSCLE 23

RESULT 3
US-09-791-477-2
; Sequence 2, Application US/09791477
; Publication No. US20030082194A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
; FILE REFERENCE: 2077.000200
; CURRENT APPLICATION NUMBER: US/09/791,477
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/184,070
; PRIOR FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 326
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-477-2

Query Match          100.0%; Score 123; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 5e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 PSQASSGQARMFPNAPYLPSCLE 23
DB      1 PSQASSGQARMFPNAPYLPSCLE 23

RESULT 4
US-09-791-477-3
; Sequence 3, Application US/09791477
; Publication No. US20030082194A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
; FILE REFERENCE: 2077.000200
; CURRENT APPLICATION NUMBER: US/09/791,477
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/184,070
; PRIOR FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 326
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 23

```

```

; TYPE: PRT
; ORGANISM: Mus musculus
US-09-791-477-3

Query Match          100.0%; Score 123; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 5e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 PSQASSGQARMFPNAPYLPSCLE 23
DB      1 PSQASSGQARMFPNAPYLPSCLE 23

RESULT 5
US-09-785-019-2
; Sequence 2, Application US/09785019
; Publication No. US20030082196A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C4
; CURRENT APPLICATION NUMBER: US/09/785,019
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-785-019-2

Query Match          100.0%; Score 123; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 5e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 PSQASSGQARMFPNAPYLPSCLE 23
DB      1 PSQASSGQARMFPNAPYLPSCLE 23

RESULT 6
US-09-785-019-3
; Sequence 3, Application US/09785019
; Publication No. US20030082196A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C4
; CURRENT APPLICATION NUMBER: US/09/785,019
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-785-019-3

Query Match          100.0%; Score 123; DB 3; Length 23;

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Best Local Similarity 100.0%; Score 123; DB 4; Length 23;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQASSGQARMFPNAPYLPSCLE 23
 DB 1 PSQASSGQARMFPNAPYLPSCLE 23

RESULT 7

US-10-125-635A-2
 ; Sequence 2, Application US/10125635A
 ; Publication No. US20030039635A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gaiger, Alexander
 ; APPLICANT: Smithgall, Molly D.
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Cheever, Martin A.
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Sutherland, R. Alec
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
 ; FILE REFERENCE: 210121.465C7
 ; CURRENT APPLICATION NUMBER: US/10/125.635A
 ; CURRENT FILING DATE: 2002-07-19
 ; NUMBER OF SEQ ID NOS: 461
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 23
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 US-10-125-635A-2

Query Match 100.0%; Score 123; DB 4; Length 23;
 Best Local Similarity 100.0%; Pred. No. 5e-11;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQASSGQARMFPNAPYLPSCLE 23
 DB 1 PSQASSGQARMFPNAPYLPSCLE 23

RESULT 8

US-10-125-635A-3
 ; Sequence 3, Application US/10125635A
 ; Publication No. US20030039635A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gaiger, Alexander
 ; APPLICANT: Smithgall, Molly D.
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Cheever, Martin A.
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Sutherland, R. Alec
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
 ; FILE REFERENCE: 210121.465C7
 ; CURRENT APPLICATION NUMBER: US/10/125.635A
 ; CURRENT FILING DATE: 2002-07-19
 ; NUMBER OF SEQ ID NOS: 461
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 3
 ; LENGTH: 23
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-10-125-635A-3

Query Match 100.0%; Score 123; DB 4; Length 23;
 Best Local Similarity 100.0%; Pred. No. 5e-11;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQASSGQARMFPNAPYLPSCLE 23
 DB 1 PSQASSGQARMFPNAPYLPSCLE 23

RESULT 9

US-10-002-603-2
 ; Sequence 2, Application US/10002603
 ; Publication No. US20030095971A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gaiger, Alexander
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Smithgall, Molly
 ; APPLICANT: Moulton, Gus
 ; APPLICANT: Vedvick, Thomas S.
 ; APPLICANT: Sleath, Paul R.
 ; APPLICANT: Moseman, Sally
 ; APPLICANT: Evans, Lawrence
 ; APPLICANT: Spies, A. Gregory
 ; APPLICANT: Boydston, Jeremy
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
 ; FILE REFERENCE: 210121.465C6
 ; CURRENT APPLICATION NUMBER: US/10/002.603
 ; CURRENT FILING DATE: 2001-10-30
 ; NUMBER OF SEQ ID NOS: 413
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 23
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 US-10-002-603-2

Query Match 100.0%; Score 123; DB 4; Length 23;
 Best Local Similarity 100.0%; Pred. No. 5e-11;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQASSGQARMFPNAPYLPSCLE 23
 DB 1 PSQASSGQARMFPNAPYLPSCLE 23

RESULT 10

US-10-002-603-3
 ; Sequence 3, Application US/10002603
 ; Publication No. US20030095971A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gaiger, Alexander
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Smithgall, Molly
 ; APPLICANT: Moulton, Gus
 ; APPLICANT: Vedvick, Thomas S.
 ; APPLICANT: Sleath, Paul R.
 ; APPLICANT: Moseman, Sally
 ; APPLICANT: Evans, Lawrence
 ; APPLICANT: Spies, A. Gregory
 ; APPLICANT: Boydston, Jeremy
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
 ; FILE REFERENCE: 210121.465C6
 ; CURRENT APPLICATION NUMBER: US/10/002.603
 ; CURRENT FILING DATE: 2001-10-30
 ; NUMBER OF SEQ ID NOS: 413
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 3
 ; LENGTH: 23
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-10-002-603-3

Query Match 100.0%; Score 123; DB 4; Length 23;
 Best Local Similarity 100.0%; Pred. No. 5e-11;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQASSGQARMFPNAPYLPSCLE 23
 DB 1 PSQASSGQARMFPNAPYLPSCLE 23

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 23, 2005, 05:09:15 ; Search time 47 Seconds
(without alignments)
40.458 Million cell updates/sec

Title: US-09-164-223-2

Sequence: 1 PSQASSGQARMPNAPYLSCLE 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA: *
1: /cgn2_6/prodata/1/1aa/5_COMB.pep: *
2: /cgn2_6/prodata/1/1aa/6_COMB.pep: *
3: /cgn2_6/prodata/1/1aa/H_COMB.pep: *
4: /cgn2_6/prodata/1/1aa/PCUS_COMB.pep: *
5: /cgn2_6/prodata/1/1aa/RE_COMB.pep: *
6: /cgn2_6/prodata/1/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	123	100.0	154	1	US-08-102-942A-5
2	123	100.0	154	2	US-09-037-179B-5
3	123	100.0	154	2	US-09-929-315-5
4	123	100.0	210	1	US-08-234-783-2
5	123	100.0	210	1	US-08-456-907-2
6	123	100.0	210	4	PCT-US95-05523-2
7	123	100.0	345	1	US-08-102-942A-2
8	123	100.0	345	2	US-09-037-179B-2
9	123	100.0	345	2	US-09-929-315-2
10	123	100.0	429	1	US-08-234-783-4
11	123	100.0	429	1	US-08-456-907-4
12	123	100.0	429	4	PCT-US95-05523-4
13	123	100.0	449	1	US-08-102-942A-4
14	123	100.0	449	1	US-08-102-942A-6
15	123	100.0	449	2	US-09-037-179B-4
16	123	100.0	449	2	US-09-037-179B-6
17	123	100.0	449	2	US-09-538-092-960
18	123	100.0	449	2	US-09-929-315-4
19	123	100.0	449	2	US-09-929-315-6
20	123	100.0	559	2	US-09-949-016-9138
21	123	100.0	559	2	US-09-949-016-9139
22	123	100.0	559	2	US-09-949-016-9140
23	123	100.0	559	2	US-09-949-016-9141
24	123	100.0	576	2	US-09-949-016-9404
25	123	100.0	576	2	US-09-949-016-9405
26	123	100.0	576	2	US-09-949-016-9406
27	123	100.0	576	2	US-09-949-016-9407

ALIGNMENTS

28	49	39.8	302	2	US-10-029-180-18	Sequence 18, Appl
29	49	39.8	340	2	US-09-328-352-7310	Sequence 7310, Ap
30	49	39.8	635	2	US-09-252-991A-23422	Sequence 23422, A
31	48	39.0	61	2	US-09-107-532A-7175	Sequence 7175, Ap
32	48	39.0	371	2	US-09-252-991A-32348	Sequence 32348, A
33	48	39.0	438	4	PCT-US95-05922A-2	Sequence 2, Appl1
34	48	39.0	618	1	US-08-511-485-8	Sequence 8, Appl1
35	48	39.0	618	2	US-09-212-971-8	Sequence 8, Appl1
36	48	39.0	618	2	US-08-800-929A-8	Sequence 8, Appl1
37	48	39.0	618	2	US-08-569-749-2	Sequence 2, Appl1
38	48	39.0	618	2	US-09-617-053A-8	Sequence 8, Appl1
39	48	39.0	618	2	US-09-069-023-29	Sequence 29, Appl
40	48	39.0	618	2	US-09-201-936-8	Sequence 8, Appl1
41	48	39.0	618	2	US-09-011-356-8	Sequence 8, Appl1
42	48	39.0	618	2	US-09-672-717-223	Sequence 223, App
43	48	39.0	618	2	US-09-201-932-8	Sequence 8, Appl1
44	48	39.0	618	2	US-09-689-366-2	Sequence 2, Appl1
45	48	39.0	618	2	US-10-232-286-2	Sequence 2, Appl1

RESULT 1
US-08-102-942A-5
Sequence 5, Application US/08102942A

Patent No. 5726288

GENERAL INFORMATION:
APPLICANT: Call, Katherine M.

APPLICANT: Glaser, Thomas M.

APPLICANT: Ito, Caryn Y.

APPLICANT: Buckler, Alan J.

APPLICANT: Pelletier, Jerry

APPLICANT: Haber, Daniel A.

APPLICANT: Rose, Elise A.

APPLICANT: Housman, David E.

APPLICANT: Breuning, Wendy

APPLICANT: Darveau, Andre

TITLE OF INVENTION: Localization and Characterization of the

TITLE OF INVENTION: Wilms' Tumor Gene

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Two Militia Drive

CITY: Lexington

STATE: Massachusetts

COUNTRY: U.S.

ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/102,942A

FILING DATE: 02-AUG-1993

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Granahan, Patricia

REGISTRATION NUMBER: 32,227

REFERENCE/DOCKET NUMBER: MIT-5194A2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-861-6240

TELEFAX: 617-861-9540

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 154 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-102-942A-5

Query Match 100.0%; Score 123; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 1.9e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQASSGQARMFPNAPYLPSCLE 23
|||||
DB 31 PSQASSGQARMFPNAPYLPSCLE 53

RESULT 2

US-09-037-179B-5
Sequence 5, Application US/09037179B

Patent No. 6316599

GENERAL INFORMATION:

APPLICANT: Call, Katherine M.

APPLICANT: Glaeser, Thomas M.

APPLICANT: Ito, Caryn Y.

APPLICANT: Buckler, Alan J.

APPLICANT: Pelletier, Jerry

APPLICANT: Haber, Daniel A.

APPLICANT: Rose, Elise A.

APPLICANT: Hausman, David E.

APPLICANT: Bruening, Wendy

APPLICANT: Darveau, Andre

TITLE OF INVENTION: Localization and Characterization of the

FILE REFERENCE: 0050.1312-011

CURRENT APPLICATION NUMBER: US/09/037,179B

CURRENT FILING DATE: 1998-03-09

PRIOR APPLICATION NUMBER: US 08/102,942

PRIOR FILING DATE: 1993-08-02

PRIOR APPLICATION NUMBER: US 07/614,161

PRIOR FILING DATE: 1990-11-13

PRIOR APPLICATION NUMBER: US 07/435,780

PRIOR FILING DATE: 1989-11-13

PRIOR APPLICATION NUMBER: US 07/795,323

PRIOR FILING DATE: 1994-09-27

NUMBER OF SEQ ID NOS: 21

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 5

LENGTH: 154

TYPE: PRT

ORGANISM: Homo sapien

US-09-037-179B-5

Query Match 100.0%; Score 123; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 1.9e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQASSGQARMFPNAPYLPSCLE 23
|||||
DB 31 PSQASSGQARMFPNAPYLPSCLE 53

RESULT 3

US-09-929-315-5
Sequence 5, Application US/09929315

Patent No. 6943011

GENERAL INFORMATION:

APPLICANT: Call, Katherine M.

APPLICANT: Glaeser, Thomas M.

APPLICANT: Ito, Caryn Y.

APPLICANT: Buckler, Alan J.

APPLICANT: Pelletier, Jerry

APPLICANT: Haber, Daniel A.

APPLICANT: Rose, Elise A.

APPLICANT: Hausman, David E.

APPLICANT: Bruening, Wendy

APPLICANT: Darveau, Andre

TITLE OF INVENTION: Localization and Characterization of the

FILE REFERENCE: 0050.1312-013

CURRENT APPLICATION NUMBER: US/09/929,315

CURRENT FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: US 09/037,179
PRIOR FILING DATE: 1998-03-09
PRIOR APPLICATION NUMBER: US 08/102,942
PRIOR FILING DATE: 1993-08-02
PRIOR APPLICATION NUMBER: US 07/614,161
PRIOR FILING DATE: 1990-11-13
PRIOR APPLICATION NUMBER: US 07/435,780
PRIOR FILING DATE: 1989-11-13
PRIOR APPLICATION NUMBER: US 07/795,323
PRIOR FILING DATE: 1991-11-20
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 154
TYPE: PRT
ORGANISM: Homo sapien
US-09-929-315-5

QY 1 PSQASSGQARMFPNAPYLPSCLE 23
|||||
DB 31 PSQASSGQARMFPNAPYLPSCLE 53

RESULT 4

US-08-234-783-2
Sequence 2, Application US/08234783

Patent No. 5622835

GENERAL INFORMATION:

APPLICANT: Herlyn, Meenhard

APPLICANT: Morris, Jennifer

APPLICANT: Rauscher III, Frank J.

APPLICANT: Rodeck, Ulrich

TITLE OF INVENTION: WTI Monoclonal Antibodies and Methods of

TITLE OF INVENTION: Use Therefor

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: Howson and Howson

STREET: Spring House Corporate Cntr, PO Box 457

CITY: Spring House

STATE: Pennsylvania

COUNTRY: USA

ZIP: 19477

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/234,783

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Bak, Mary E.

REGISTRATION NUMBER: 31,215

REFERENCE/DOCKET NUMBER: WST48USA

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-540-9200

TELEFAX: 215-540-5818

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 210 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-234-783-2

Query Match 100.0%; Score 123; DB 1; Length 210;
Best Local Similarity 100.0%; Pred. No. 2.7e-11;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PSQASSGQARMFPNAPYLPSCLE 23
128 PSQASSGQARMFPNAPYLPSCLE 150

RESULT 5

US-08-456-907-2
Sequence 2, Application US/08456907
Patent No. 5633142
GENERAL INFORMATION:
APPLICANT: Herlyn, Meenhard
APPLICANT: Morrie, Jennifer
APPLICANT: Rauscher III, Frank J.
APPLICANT: Rodeck, Ulrich
TITLE OF INVENTION: Wt1 Monoclonal Antibodies and Methods of
TITLE OF INVENTION: Use Therefor
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,907
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/234,783
FILING DATE: 28-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST48AUSA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 210 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-456-907-2

Query Match 100.0%; Score 123; DB 1; Length 210;
Best Local Similarity 100.0%; Pred. No. 2.7e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQASSGQARMFPNAPYLPSCLE 23
128 PSQASSGQARMFPNAPYLPSCLE 150

RESULT 6

PCT-US95-05523-2
Sequence 2, Application PC/TUS9505523
GENERAL INFORMATION:
APPLICANT: The Wistar Institute of Anatomy and Biology
TITLE OF INVENTION: Wt1 Monoclonal Antibodies and
TITLE OF INVENTION: Methods of Use Therefor
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, PO Box 457

CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05523
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/234,783
FILING DATE: 28-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST48PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 210 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-05523-2

Query Match 100.0%; Score 123; DB 4; Length 210;
Best Local Similarity 100.0%; Pred. No. 2.7e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQASSGQARMFPNAPYLPSCLE 23
128 PSQASSGQARMFPNAPYLPSCLE 150

RESULT 7

US-08-102-942A-2
Sequence 2, Application US/08102942A
Patent No. 5726288
GENERAL INFORMATION:
APPLICANT: Call, Katherine M.
APPLICANT: Glaser, Thomas M.
APPLICANT: Ito, Caryn Y.
APPLICANT: Buckler, Alan J.
APPLICANT: Pelletier, Jerry
APPLICANT: Haber, Daniel A.
APPLICANT: Rose, Elise A.
APPLICANT: Housman, David E.
APPLICANT: Bruening, Wendy
APPLICANT: Darveau, Andre
TITLE OF INVENTION: Localization and Characterization of the
TITLE OF INVENTION: Wilms' Tumor Gene
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: U.S.
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/102,942A
FILING DATE: 02-AUG-1993

NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: MST48USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 429 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-234-783-4

Query Match 100.0%; Score 123; DB 1; Length 429;
Best Local Similarity 100.0%; Pred. No. 6e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQASSGQARMPNAPYLPSCLE 23
DB 117 PSQASSGQARMPNAPYLPSCLE 139

RESULT 11
US-08-456-907-4
Sequence 4, Application US/08456907
Patent No. 5633142
GENERAL INFORMATION:
APPLICANT: Herlyn, Meenhard
APPLICANT: Morris, Jennifer
APPLICANT: Rauscher III, Frank J.
APPLICANT: Rodeck, Ulrich
TITLE OF INVENTION: WT1 Monoclonal Antibodies and Methods of
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,907
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/234,783
FILING DATE: 28-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: MST48AUSA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 429 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-456-907-4

Query Match 100.0%; Score 123; DB 1; Length 429;
Best Local Similarity 100.0%; Pred. No. 6e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSQASSGQARMPNAPYLPSCLE 23
DB 117 PSQASSGQARMPNAPYLPSCLE 139

RESULT 12
PCT-US95-05523-4
Sequence 4, Application PC/TUS9505523
GENERAL INFORMATION:
APPLICANT: The Wistar Institute of Anatomy and Biology
TITLE OF INVENTION: WT1 Monoclonal Antibodies and
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05523
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/234,783
FILING DATE: 28-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: MST48PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 429 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-05523-4

Query Match 100.0%; Score 123; DB 4; Length 429;
Best Local Similarity 100.0%; Pred. No. 6e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 117 PSQASSGQARMPNAPYLPSCLE 139

RESULT 13
US-08-102-942A-4
Sequence 4, Application US/08102942A
Patent No. 5726288
GENERAL INFORMATION:
APPLICANT: Call, Katherine M.
APPLICANT: Glaser, Thomas M.
APPLICANT: Ito, Caryn Y.
APPLICANT: Buckler, Alan J.
APPLICANT: Pelletier, Jerry
APPLICANT: Haber, Daniel A.
APPLICANT: Rose, Elise A.
APPLICANT: Housman, David E.
APPLICANT: Bruneau, Wendy
APPLICANT: Darveau, Andre
TITLE OF INVENTION: Localization and Characterization of the
Wilms' Tumor Gene

NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: U.S.
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/102,942A
FILING DATE: 02-AUG-1993
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-5194A2
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 449 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-102-942A-4

Query Match 100.0%; Score 123; DB 1; Length 449;
Best Local Similarity 100.0%; Pred. No. 6.3e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSQASSGQARMPNAPYLPSCLE 23
Db 117 PSQASSGQARMPNAPYLPSCLE 139

RESULT 14
US-08-102-942A-6
Sequence 6, Application US/08102942A
Patent No. 5726288
GENERAL INFORMATION:
APPLICANT: Call, Katherine M.
APPLICANT: Glaser, Thomas M.
APPLICANT: Ito, Caryn Y.
APPLICANT: Buckler, Alan J.
APPLICANT: Pelletier, Jerry
APPLICANT: Haber, Daniel A.
APPLICANT: Rose, Elise A.
APPLICANT: Housman, David E.
APPLICANT: Bruening, Wendy
APPLICANT: Darveau, Andre
TITLE OF INVENTION: Localization and Characterization of the
TITLE OF INVENTION: Wilms' Tumor Gene
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: U.S.
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/102,942A

FILING DATE: 02-AUG-1993
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-5194A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 449 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-102-942A-6

Query Match 100.0%; Score 123; DB 1; Length 449;
Best Local Similarity 100.0%; Pred. No. 6.3e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSQASSGQARMPNAPYLPSCLE 23
Db 117 PSQASSGQARMPNAPYLPSCLE 139

RESULT 15
US-09-037-179B-4
Sequence 4, Application US/09037179B
Patent No. 6316599
GENERAL INFORMATION:
APPLICANT: Call, Katherine M.
APPLICANT: Glaser, Thomas M.
APPLICANT: Ito, Caryn Y.
APPLICANT: Buckler, Alan J.
APPLICANT: Pelletier, Jerry
APPLICANT: Haber, Daniel A.
APPLICANT: Rose, Elise A.
APPLICANT: Housman, David E.
APPLICANT: Bruening, Wendy
APPLICANT: Darveau, Andre
TITLE OF INVENTION: Localization and Characterization of the
TITLE OF INVENTION: Wilms' Tumor Gene
FILE REFERENCE: 0050,1312-011
CURRENT APPLICATION NUMBER: US/09/037,179B
CURRENT FILING DATE: 1998-03-09
PRIOR APPLICATION NUMBER: US 08/102,942
PRIOR FILING DATE: 1993-08-02
PRIOR APPLICATION NUMBER: US 07/614,161
PRIOR FILING DATE: 1990-11-13
PRIOR APPLICATION NUMBER: US 07/435,780
PRIOR FILING DATE: 1989-11-13
PRIOR APPLICATION NUMBER: US 07/795,323
PRIOR FILING DATE: 1994-09-27
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 449
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Murine
US-09-037-179B-4

Query Match 100.0%; Score 123; DB 2; Length 449;
Best Local Similarity 100.0%; Pred. No. 6.3e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PSQASSGQARMPNAPYLPSCLE 23
Db 117 PSQASSGQARMPNAPYLPSCLE 139

2 Fri Nov 25 17:46:07 2005

us-09-164-223-2.ra1

Page 7

Search completed: November 23, 2005, 05:18:06
Job time : 47 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 23, 2005, 05:17:31 ; Search time 8 Seconds
(without alignments)

8.714 Million cell updates/sec

Title: US-09-164-223-2

Perfect score: 123
Sequence: 1 PSQASSGQARFPPNAPYLPSCLE 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 17545 seqs, 3030971 residues

Total number of hits satisfying chosen parameters: 17545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43.5	35.4	32	1	US-10-945-853-9
2	43.5	35.4	188	1	US-10-945-853-1
3	43.5	35.4	188	1	US-10-945-853-2
4	42	34.1	101	1	US-10-793-626-926
5	41	33.3	2630	7	US-11-186-731-2
6	41	33.3	7968	7	US-11-186-731-5
7	38	30.9	249	7	US-11-054-515-714
8	38	30.9	249	7	US-11-054-515-738
9	38	30.9	249	7	US-11-054-515-760
10	38	30.9	318	1	US-10-821-234-1117
11	38	30.9	1970	1	US-10-821-234-1641
12	37.5	30.5	216	1	US-10-667-295-105
13	37.5	30.5	282	1	US-10-667-295-104
14	37	30.1	147	1	US-10-793-626-2238
15	37	30.1	247	1	US-10-131-826A-284
16	37	30.1	249	7	US-11-054-515-388
17	37	30.1	249	7	US-11-054-515-430
18	37	30.1	249	7	US-11-054-515-470
19	37	30.1	249	7	US-11-054-515-769
20	37	30.1	344	1	US-10-821-234-911
21	36	29.3	543	1	US-10-495-664-3
22	36	29.3	14	7	US-11-054-515-2371
23	36	29.3	249	7	US-11-054-515-371
24	36	29.3	249	7	US-11-054-515-593
25	36	29.3	397	1	US-10-828-033-25

25	36	29.3	398	1	US-10-828-033-23	Sequence 23, Appl
27	36	29.3	462	1	US-10-828-033-24	Sequence 24, Appl
28	36	29.3	462	1	US-10-821-234-1548	Sequence 1548, Ap
29	36	29.3	613	1	US-10-131-826A-190	Sequence 190, Ap
30	36	29.3	867	1	US-10-131-826A-20	Sequence 20, Appl
31	36	29.3	14	7	US-11-054-515-2388	Sequence 2388, Ap
32	35	28.5	14	7	US-11-054-515-2610	Sequence 2610, Ap
33	35	28.5	14	7	US-11-054-515-2613	Sequence 2613, Ap
34	35	28.5	14	7	US-11-054-515-2615	Sequence 2615, Ap
35	35	28.5	249	7	US-11-054-515-489	Sequence 489, App
36	35	28.5	249	7	US-11-054-515-666	Sequence 666, App
37	35	28.5	249	7	US-11-054-515-717	Sequence 717, App
38	35	28.5	249	7	US-11-054-515-736	Sequence 736, App
39	35	28.5	249	7	US-11-054-515-754	Sequence 754, App
40	35	28.5	406	1	US-10-821-234-1026	Sequence 1026, Ap
41	35	28.5	501	1	US-10-971-560-2	Sequence 2, Appl
42	35	28.5	501	1	US-10-971-560-10	Sequence 10, Appl
43	35	28.5	3056	7	US-11-109-156-20	Sequence 20, Appl
44	34	27.6	14	7	US-11-054-515-2603	Sequence 2603, Ap
45	34	27.6	14	7	US-11-054-515-2672	Sequence 2672, Ap

ALIGNMENTS

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RESULT 1
US-10-945-853-9
; Sequence 9, Application US/10945853
; Publication No. US20050255117A1
; GENERAL INFORMATION:
; APPLICANT: Biogen, Inc.
; APPLICANT: Sanicola-Nadel, Michele
; APPLICANT: Adkins, Heather
; APPLICANT: Miklasz, Steven Donald
; APPLICANT: Rayhorn, Paul
; APPLICANT: Schiffer, Susan Gail
; APPLICANT: Williams, Kevin
; TITLE OF INVENTION: Cripco-Specific Antibodies
; FILE REFERENCE: BGNAL17CPCCN
; CURRENT APPLICATION NUMBER: US/10/945,853
; CURRENT FILING DATE: 2004-09-20
; PRIOR APPLICATION NUMBER: PCT/US02/31462
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: PCT/US02/11950
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/286,782
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/293,020
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/301,091
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/367,002
; PRIOR FILING DATE: 2002-03-22
; NUMBER OF SEQ ID NOS: 9
; SEQ ID NO 9
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Mod_res
; LOCATION: 1
; OTHER INFORMATION: N-terminal acetylation
US-10-945-853-9
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Query Match 35.4%; Score 43.5; DB 1; Length 32;
Best Local Similarity 60.0%; Pred. No. 0.26;
Matches 9; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

QY 7 GOARFPPNAPYLPSC 21
DB 18 GQLRCFPPA-FLPSC 31

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RESULT 2
US-10-945-853-1
; Sequence 1, Application US/10945853
; Publication No. US20050255117A1
; GENERAL INFORMATION:
; APPLICANT: Biogen, Inc.
; APPLICANT: Sanicola-Nedel, Michele
; APPLICANT: Adkins, Heather
; APPLICANT: Miklasz, Steven Donald
; APPLICANT: Rayhorn, Paul
; APPLICANT: Schiffer, Susan Gail
; APPLICANT: Williams, Kevin
; TITLE OF INVENTION: Crypto-Specific Antibodies
; FILE REFERENCE: BGN117CPCCN
; CURRENT APPLICATION NUMBER: US/10/945,853
; CURRENT FILING DATE: 2004-09-20
; PRIOR APPLICATION NUMBER: PCT/US02/31462
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: PCT/US02/11950
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/286,782
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/293,020
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/301,091
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/367,002
; PRIOR FILING DATE: 2002-03-22
; NUMBER OF SEQ ID NOS: 9
; SEQ ID NO 1
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-945-853-1

Query Match          35.4%; Score 43.5; DB 1; Length 188;
Best Local Similarity 60.0%; Pred. No. 1.7;
Matches 9; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

Cy 7 GQARMPNAPYLPSCL 21
Db 136 GQLRCFPOA-FLPGC 149

RESULT 3
US-10-945-853-2
; Sequence 2, Application US/10945853
; Publication No. US20050255117A1
; GENERAL INFORMATION:
; APPLICANT: Biogen, Inc.
; APPLICANT: Sanicola-Nedel, Michele
; APPLICANT: Adkins, Heather
; APPLICANT: Miklasz, Steven Donald
; APPLICANT: Rayhorn, Paul
; APPLICANT: Schiffer, Susan Gail
; APPLICANT: Williams, Kevin
; TITLE OF INVENTION: Crypto-Specific Antibodies
; FILE REFERENCE: BGN117CPCCN
; CURRENT APPLICATION NUMBER: US/10/945,853
; CURRENT FILING DATE: 2004-09-20
; PRIOR APPLICATION NUMBER: PCT/US02/31462
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: PCT/US02/11950
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/286,782
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/293,020
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/301,091
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/367,002
; PRIOR FILING DATE: 2002-03-22
; NUMBER OF SEQ ID NOS: 9
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; SEQ ID NO 2
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-945-853-2

Query Match          35.4%; Score 43.5; DB 1; Length 188;
Best Local Similarity 60.0%; Pred. No. 1.7;
Matches 9; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

Cy 7 GQARMPNAPYLPSCL 21
Db 136 GQLRCFPOA-FLPGC 149

RESULT 4
US-10-793-626-926
; Sequence 926, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P03480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 926
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-793-626-926

Query Match          34.1%; Score 42; DB 1; Length 101;
Best Local Similarity 45.0%; Pred. No. 1.5;
Matches 9; Conservative 4; Mismatches 5; Indels 2; Gaps 1;

Cy 5 SSGQARMPNAPYLPSCL 22
Db 9 NSGLSVAFPNVTPYLPNAM 28

RESULT 5
US-11-186-731-2
; Sequence 2, Application US/11186731
; Publication No. US20050255521A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Acton, Susan L.
; TITLE OF INVENTION: 59079 and 12599, Protein Kinase Family
; TITLE OF INVENTION: Members and Uses Therefor
; FILE REFERENCE: MP12001-047P1PCP1(M)
; CURRENT APPLICATION NUMBER: US/11/186,731
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/077,130
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 60/269201
; PRIOR FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 2630
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-186-731-2

Query Match          33.3%; Score 41; DB 7; Length 2630;
Best Local Similarity 43.8%; Pred. No. 64;
```

Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 PSQASSGQARMPNAP 16
 ||:|||||
 DB 1636 PSEACGCAQRLLPSAP 1651

RESULT 6
 US-11-186-731-5
 ; Sequence 5, Application US/11186731
 ; Publication No. US20050255521A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kapeller-Libermann, Roseana
 ; APPLICANT: Acton, Susan L.
 ; TITLE OF INVENTION: 59079 and 12599, Protein Kinase Family
 ; FILE REFERENCE: MP12001-047P1RCPI(M)
 ; CURRENT APPLICATION NUMBER: US/11/186,731
 ; CURRENT FILING DATE: 2005-07-21
 ; PRIOR APPLICATION NUMBER: US/10/077,130
 ; PRIOR FILING DATE: 2002-02-15
 ; PRIOR APPLICATION NUMBER: 60/269201
 ; PRIOR FILING DATE: 2001-02-15
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 5
 ; LENGTH: 7968
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-186-731-5

Query Match 33.3%; Score 41; DB 7; Length 7968;
 Best Local Similarity 43.8%; Pred. No. 2.1e+02;
 Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 PSQASSGQARMPNAP 16
 ||:|||||
 DB 6974 PSEACGCAQRLLPSAP 6989

RESULT 7
 US-11-054-515-714
 ; Sequence 714, Application US/11054515
 ; Publication No. US20050255532A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 ; FILE REFERENCE: PF523P3
 ; CURRENT APPLICATION NUMBER: US/11/054,515
 ; CURRENT FILING DATE: 2005-02-10
 ; PRIOR APPLICATION NUMBER: 60/543,296
 ; PRIOR FILING DATE: 2004-02-11
 ; PRIOR APPLICATION NUMBER: 60/580,347
 ; PRIOR FILING DATE: 2004-06-18
 ; PRIOR APPLICATION NUMBER: 10/293,418
 ; PRIOR FILING DATE: 2002-11-14
 ; PRIOR APPLICATION NUMBER: 60/331,469
 ; PRIOR FILING DATE: 2001-11-16
 ; PRIOR APPLICATION NUMBER: 60/340,817
 ; PRIOR FILING DATE: 2001-12-19
 ; PRIOR APPLICATION NUMBER: 09/880,748
 ; PRIOR FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: 60/293,499
 ; PRIOR FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: 60/277,379
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/276,248
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/240,816
 ; PRIOR FILING DATE: 2000-10-17
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 3247
 ; SEQ ID NO 714

LENGTH: 249
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-054-515-714

Query Match 30.9%; Score 38; DB 7; Length 249;
 Best Local Similarity 50.0%; Pred. No. 15;
 Matches 8; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 4 ASSGQARMPNAPYLP 19
 ||:|||||
 DB 97 ARSRDLLFPNAPLSP 112

RESULT 8
 US-11-054-515-738
 ; Sequence 738, Application US/11054515
 ; Publication No. US20050255532A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 ; FILE REFERENCE: PF523P3
 ; CURRENT APPLICATION NUMBER: US/11/054,515
 ; CURRENT FILING DATE: 2005-02-10
 ; PRIOR APPLICATION NUMBER: 60/543,296
 ; PRIOR FILING DATE: 2004-02-11
 ; PRIOR APPLICATION NUMBER: 60/580,347
 ; PRIOR FILING DATE: 2004-06-18
 ; PRIOR APPLICATION NUMBER: 10/293,418
 ; PRIOR FILING DATE: 2002-11-14
 ; PRIOR APPLICATION NUMBER: 60/331,469
 ; PRIOR FILING DATE: 2001-11-16
 ; PRIOR APPLICATION NUMBER: 60/340,817
 ; PRIOR FILING DATE: 2001-12-19
 ; PRIOR APPLICATION NUMBER: 09/880,748
 ; PRIOR FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: 60/293,499
 ; PRIOR FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: 60/277,379
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/276,248
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/240,816
 ; PRIOR FILING DATE: 2000-10-17
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 3247
 ; SEQ ID NO 738
 ; LENGTH: 249
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-054-515-738

Query Match 30.9%; Score 38; DB 7; Length 249;
 Best Local Similarity 50.0%; Pred. No. 15;
 Matches 8; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 4 ASSGQARMPNAPYLP 19
 ||:|||||
 DB 97 ARSRDLLFPNAPLSP 112

RESULT 9
 US-11-054-515-760
 ; Sequence 760, Application US/11054515
 ; Publication No. US20050255532A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 ; FILE REFERENCE: PF523P3
 ; CURRENT APPLICATION NUMBER: US/11/054,515
 ; CURRENT FILING DATE: 2005-02-10
 ; PRIOR APPLICATION NUMBER: 60/543,296
 ; PRIOR FILING DATE: 2004-02-11

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; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO: 760
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-760

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Query Match      30.9%; Score 38; DB 7; Length 249;
Best Local Similarity 50.0%; Pred. No. 15;
Matches 8; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

```

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QY      4  ASSGQARMFPNAPYLP 19
DB      97 ARSRDLLEFPNPLSP 112

```

```

RESULT 10
US-10-821-234-1117
; Sequence 1117, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1117
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1117

```

```

Query Match      30.9%; Score 38; DB 1; Length 318;
Best Local Similarity 40.9%; Pred. No. 20;
Matches 9; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

```

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QY      1  PSQASSGQARMFPNAPYLPSC 22
DB      45 PPAPAPRRPSPRAVMLPLCL 66

```

```

RESULT 11
US-10-821-234-1641
; Sequence 1641, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan

```

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; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1641
; LENGTH: 1970
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1641

```

```

Query Match      30.9%; Score 38; DB 1; Length 1970;
Best Local Similarity 40.0%; Pred. No. 1.4e+02;
Matches 8; Conservative 4; Mismatches 6; Indels 2; Gaps 1;

```

```

QY      1  PSQASSGQARMFPNAPYLP 20
DB      1567 PTPSPGSPG--PSSPYTPS 1564

```

```

RESULT 12
US-10-667-295-105
; Sequence 105, Application US/10667295
; Publication No. US20050257293A1
; GENERAL INFORMATION:
; APPLICANT: Mascia, Peter
; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
; FILE REFERENCE: 11696-047001
; CURRENT APPLICATION NUMBER: US/10/667,295
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,823
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 263
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 105
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (2)...(216)
; OTHER INFORMATION: Ceres Seq. ID no. 12431633
US-10-667-295-105

```

```

Query Match      30.5%; Score 37.5; DB 1; Length 216;
Best Local Similarity 34.8%; Pred. No. 16;
Matches 8; Conservative 6; Mismatches 6; Indels 3; Gaps 1;

```

```

QY      2  SQASSGQARMFPNAPYLP---PSC 21
DB      28 STTSGKFKMFPKSNKFSMFPSC 50

```

```

RESULT 13
US-10-667-295-104
; Sequence 104, Application US/10667295
; Publication No. US20050257293A1
; GENERAL INFORMATION:
; APPLICANT: Mascia, Peter
; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
; FILE REFERENCE: 11696-047001
; CURRENT APPLICATION NUMBER: US/10/667,295
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,823
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 263
; SOFTWARE: FastSeq for Windows Version 4.0

```

APPLICANT: Zhang, Zemin

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